

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 10:53:51 ; Search time 166 Seconds

(without alignments)
687.836 Million cell updates/sec

Title: US-08-989-881-2
Perfect score: 1419
Sequence: 1 MANQTQSDXVILGRELGRG.....TKRLTAQQVLDHPWQNAKK 274

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1859788 seqs, 416717961 residues

Total number of hits satisfying chosen parameters: 1859788

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10F_PUBCOMB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1419	100.0	274	15	US-10-243-581B-1
2	1318	92.9	274	15	US-10-243-581B-3
3	1252	88.2	536	15	US-10-424-599-180685
4	1246	87.8	535	15	US-10-425-114-45800
5	1164	82.0	533	15	US-10-424-599-200299
6	1155	81.4	550	16	US-10-437-963-109887
7	1147	80.8	553	15	US-10-425-114-68288
8	1143	80.5	539	16	US-10-425-115-213591
9	1143	80.5	553	15	US-10-425-114-67473
10	1136	80.1	538	16	US-10-425-115-198373
11	1136	80.1	592	15	US-10-425-114-65930

12	1136	80.1	592	15	US-10-425-114-70054	Sequence 70054, A
13	1135	80.0	425	16	US-10-767-701-44784	Sequence 44784, A
14	1132	79.8	589	16	US-10-437-963-160820	Sequence 160820, A
15	1115	78.6	661	16	US-10-437-963-163957	Sequence 163957, A
16	1101	77.6	541	16	US-10-425-114-57084	Sequence 57084, A
17	1084	76.4	612	16	US-10-437-963-199098	Sequence 199098, A
18	1064.5	75.0	531	16	US-10-425-115-231166	Sequence 231166, A
19	1064.5	75.0	540	15	US-10-425-114-49937	Sequence 49937, A
20	1064.5	75.0	545	15	US-10-425-114-53691	Sequence 53691, A
21	1062	74.8	465	15	US-10-425-114-49938	Sequence 49938, A
22	1048	73.9	503	16	US-10-425-115-214199	Sequence 214199, A
23	1041	73.4	563	16	US-10-437-963-186792	Sequence 186792, A
24	1018.5	71.8	535	15	US-10-424-599-254375	Sequence 254375, A
25	947	66.7	549	9	US-09-828-313-39	Sequence 39, Appl
26	947	66.7	549	16	US-10-768-8638-39	Sequence 39, Appl
27	932	65.7	595	16	US-10-437-963-141791	Sequence 141791, A
28	926	65.3	470	15	US-10-425-114-70198	Sequence 70198, A
29	926	65.3	639	9	US-09-854-731-17	Sequence 17, Appl
30	926	65.3	640	16	US-10-425-115-340679	Sequence 340679, A
31	916	64.6	413	15	US-10-243-581B-2	Sequence 2, Appl
32	916	64.6	612	16	US-10-437-963-139689	Sequence 139689, A
33	914.5	64.4	578	16	US-10-437-963-134013	Sequence 134013, A
34	910	64.1	513	16	US-10-437-963-173217	Sequence 173217, A
35	910	64.1	546	15	US-10-424-599-203557	Sequence 203557, A
36	910	64.1	549	15	US-10-425-114-54704	Sequence 54704, A
37	910	64.1	583	15	US-10-425-114-45048	Sequence 45048, A
38	909.5	64.1	518	16	US-10-437-963-168927	Sequence 168927, A
39	906	63.8	582	16	US-10-425-115-228630	Sequence 228630, A
40	900	63.4	341	16	US-10-437-963-161238	Sequence 161238, A
41	899	63.4	355	16	US-10-767-701-45463	Sequence 45463, A
42	898	63.3	549	16	US-10-437-963-164372	Sequence 164372, A
43	897	63.2	568	16	US-10-437-963-204568	Sequence 204568, A
44	896.5	63.2	577	16	US-10-437-963-131419	Sequence 131419, A
45	896	63.1	578	16	US-10-437-963-111277	Sequence 111277, A

ALIGNMENTS

RESULT 1
US-10-243-581B-1
; Sequence 1, Application US/10243581B
; Publication No. US20030219763A1
; GENERAL INFORMATION:
; APPLICANT: Sheen, Jen
; TITLE OF INVENTION: Plant Protoplast Gene Expression Systems
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: 00786/386002
; CURRENT APPLICATION NUMBER: US/10/243,581B
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: PCT/US01/07999
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: US 60/189,074
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 08/989,881
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: US 60/032,966
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: US 09/371,338
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/095,938
; PRIOR FILING DATE: 1998-08-10
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-243-581B-1

Query Match 100.0%; Score 1419; DB 15; Length 274;
Best Local Similarity 100.0%; Pred. No. 1.3e-108;
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MANOTOISDKYILGRELGRGFGITYILCTDRETRALACKSISKBLRTAVDVEDVRREV	50
Db	1	MANOTOISDKYILGRELGRGFGITYILCTDRETRALACKSISKBLRTAVDVEDVRREV	60
Qy	61	TIMSTLPEHPNVVLKATYENETVHLYMELCEGGELFGRI VARGHYTERAAATVARTTA	120
Db	61	TIMSTLPEHPNVVLKATYENETVHLYMELCEGGELFGRI VARGHYTERAAATVARTTA	120
Qy	121	EVVRMCHVGMVHRDLKPENFLFANKENSALKAI DFGLSVLFKPGERFTEIVGSPYYMA	180
Db	121	EVVRMCHVGMVHRDLKPENFLFANKENSALKAI DFGLSVLFKPGERFTEIVGSPYYMA	180
Qy	181	PEVLKRNYPGEVDVMSAGVIYILLCGVPPFWAETEQQVALAILRGVLDFKDDPWSQISE	240
Db	181	PEVLKRNYPGEVDVMSAGVIYILLCGVPPFWAETEQQVALAILRGVLDFKDDPWSQISE	240
Qy	241	SAKSLVKOMLEPDSFKRLTAQQVLDPHPMIONAKK	274
Db	241	SAKSLVKOMLEPDSFKRLTAQQVLDPHPMIONAKK	274

RESULT 2

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US-10-243-581B-3
; Sequence 3, Application US/10243581B
; Publication No. US20030219763A1
; GENERAL INFORMATION:
; APPLICANT: Sheen, Jen
; TITLE OF INVENTION: Plant Protoplast Gene
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: 00786/386002
; CURRENT APPLICATION NUMBER: US/10/243,581B
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: PCT/US01/07999
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: US 60/189,074
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 08/989,881
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: US 60/032,966
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: US 09/371,338
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/095,938
; PRIOR FILING DATE: 1998-08-10
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-243-581B-3

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Query Match	Score	DB	Length
Best Local Similarity	92.9%	1318	274
Matches 252; Conservative	92.0%	Pred. No. 2.6e-100	
Matches 252; Conservative	8	Mismatches 14	Indels 0
Matches 252; Conservative	8	Mismatches 14	Indels 0
Matches 252; Conservative	8	Mismatches 14	Indels 0

Qy	1	MANOTQISDKYILGREIGRGFBGITYLCTDRETREALACKSISKRKLRTAVDVEDVREV	60
Db	1	MSNOTQISDKYILGREIGRGFBGITYLCTDRETREALACKSISKRKLRTAVDIEDVREV	60
Qy	61	TIINSTLPEHPNVVKLKYEDNETVHLWMEICGEGELFGRIVARGHYTERRAAATVARTIA	120
Db	61	AIINSTLPEHPNVVKLKASYENENVHLWMEICGEGELFDRIVARGHYTERRAAAAVARTIA	120
Qy	121	EVVRMCHVNGVWHRDLKPENELFANKKENSALKADFGLSVLFKPGKPFTEIVGSPYYMA	180
Db	121	EVVVMCHSNGVWHRDLKPENELFANKKENSPLKADFGLSVFFKSGDKFTEIVGSPYYMA	180
Qy	181	PEVLKRNYPGEVDVWSAGVIYILLCGVPPFWAETEQGVALAILRGVILDFKRDPMQSQISE	240
Db	181	PEVLKRDYGPGEVDVWSAGVIYILLCGAPFWAETEQGVALAILRGVILDFKRDPMQSQISE	240

[illegible]

Query Match	88.2%	Score 1252;	DB 15;	Length 536;
Best Local Similarity	86.1%;	Pred. No. 1.6e-94;		
Matches 236;	Conservative	17;	Mismatches 21;	Indels 0;
Gaps	0;			

Qy	1	MANOTQISDKYIIIGRELGRGEFGITYICTDRETREALACKSISKRKLRTAVDVEDVVRREV	50
Db	47	VTSRSLGDKYVIGRELGRGEFGITYICTDRETQOELACKSISKRKLRTAIDVEDVVRREV	106
Qy	61	TIINSTLPEHNNVVKLKATYEDNETVHVLVMELCGGELFGRIVARGHYTERAAATVARTIA	120
Db	107	AINSTLPEHANVVKLKATYEDNEENVHVLVMELCAGGELFDRIVARGHYSERAAANVARTIA	166
Qy	121	EVVRMCHVNGVMHRDLKPENFLFANKKENSALKAIIDFGLSVLPKPGERFTEIVGSPYYNA	180
Db	167	EVVRMCHANGVMHRDLKPENFLFANKKENSVLKAIIDFGLCVFFIPGGERFLEIVGSPYYNA	226
Qy	181	PEVLKRNYPGEVDVWSAGVITYIILCCGVPFFWAEQGVALAILRGVLUDFKRDPWQSQISE	240
Db	227	PEVLKRNYPGEVDVWSAGVITYIILCCGVPFFWAEQGVALAILRGVLUDFKRDPWQSQISE	286
Qy	241	SAKSLVKQMLEPDPSTKRLTAAQVLDHPWIQNAKK	274
Db	287	SAKSLVRLMLEPDPKRLRTAEQVLEHPWLQNAKK	320

RESULT 4
US-10-425-114-45800
; Sequence 45800, Application US/10425114
; Publication No. US20040034888A1

```

: GENERAL INFORMATION:
:
: APPLICANT: Liu, Jingdong
:
: APPLICANT: Zhou, Yihua
:
: APPLICANT: Kovalic, David K.
:
: APPLICANT: Screen, Steven E.
:
: APPLICANT: Tabaska, Jack E.
:
: APPLICANT: Cao, Yongwei
:
: TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
:
: TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
:
: FILE REFERENCES: 38-21(53313)B
:
: CURRENT APPLICATION NUMBER: US/10/425,114
:
: CURRENT FILING DATE: 2003-04-28

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APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

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QY 127 HVGVMHRDLKPENFLFANKKENSALKAIDFGLSVLFGPGRFRFTI VGSPPYMAPEVLKR 186
DB 180 HKHGVMRDLKPENFLFANKKESAAALKAIDFGLSVFFTPGRFSBI VGSPPYMAPEVLKR 239
QY 187 NYGPEVDWMSAGVLYILLCGVPFPFAETEOGVALAILRGLVDK RDPWSQISESAKSILV 246
DB 240 NYGPEVDWMSAGVLYILLCGVPFPFAETEOGVAAIIRSVIDPK RDPWPVRVSDNAKDLV 299
QY 247 KQMLEPDSRKRLTAQQVLDPHPIQNAKK 274
DB 300 RGMNLNPDPKRLTAHQVLGHPWLQNIKK 327

RESULT 9
US-10-425-114-67473
; Sequence 67473, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 67473
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4757-010-H10_FU1.pgp
US-10-425-114-67473

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Query Match	80.5%	Score 1143;	DB 15;	Length 553;
Best Local Similarity	80.2%;	Pred. No. 1.5e-85;		
Matches 215;	Conservative 23;	Mismatches 30;	Indels 0;	Gaps 0;
Qy	7	ISDKYILGRELGRGEFGITVCTDRTREALACKSISKRLKRTAVDVEDVREVTIMSTL	66	
Db	74	IAARYELGAELGRGEFGVTVCTDRASGEALACKSISKRLKRTAVDLEDVREVEIMRHL	133	
Qy	67	PEHPNVVVKATYEDNETVLMVLCGGELFGRIVARGHYTERAAATVARTIAEVVRMC	126	
Db	134	PKHPNVVTLRDTYEDDNNAVLVLMVLCGGELFORIVARGHYTERAAALVLRITVEVQMC	193	
Qy	127	HVNGVMHRDLKPNFLFANKKENSALKAIDFGLSVLFKPGERFTEIVGSPYYMAPEVLKR	186	
Db	194	HKHGVNHRDLKPNFLFANKKESAAALKAIIDFGLSVFTPTGERFSEIVGSPYYMAPEVLKR	253	
Qy	187	NYGPEVDVWSAGVILYILLCGVPFPFMAETBQGVALAILRGVLDPKRPDQWSQISAKSLV	246	
Db	254	NYGPEVDVWSAGVILYILLCGVPFPFMAETBQGVAAIIRSVIDPKRPDPWPRVSDNADLV	313	
Qy	247	KQMLEPDSITKRLTAQQVLDPHPWTONAKK	274	
Db	314	RGLMNPDPKRLTAHQVLGHPWLTQNTKK	341	

DB 314 RGMNPDPKRRLTAHQVLGHPWLQNK 341
 RESULT 10
 US-10-425-115-198373
 ; Sequence 198373, Application US/10425115
 ; Publication No, US20040214272A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With


```

; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 198373
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Zea mays
; NAME/KEY: unsure
; LOCATION: (1)..(538)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_112494C.1.pep
; US-10-425-115-198373

Query Match      80.1%; Score 1136; DB 16; Length 538;
Best Local Similarity 79.1%; Pred. No. 5.6e-85;
Matches 212; Conservative 26; Mismatches 30; Indels 0; Gaps 0;

Qy 7 ISDKYILGRELGRGEGFITYLCTDRETREALACKSISKRLRTAVDVEDVRREVTIMSTL 66
Db 58 IDDKYVLDRELGRGEGFITYLCTDRETREALACKSISKRLRTAVDVEDVRREVTIMSTL 117

Qy 67 PEHPNVVKLKATYEDNETVHLMELCEGGELFGRIVARGHYTERAAATVARTIAEVVRMC 126
Db 118 PKSPSVLSREACEDDGAHVLMELCEGGELFGRIVARGHYTERAAASVTRTILEVVOLC 177

Qy 127 HVGVMHRDLKPENFLFANKKENSALKAIIDFGLSVLPKPGERFTEIVGSPYYMAPEVLKR 186
Db 178 HRHGVHHRDLKPENFLFANKKENSPLKAIIDFGLSIFPKGKEFSEIVGSPYYMAPEVLKR 237

Qy 187 NYGPEVDVMSAGVILYILLCGVPPFWAETEGQVALAILRGVLDPKRDPWQISSEAKSLV 246
Db 238 NYGPEIDWSAGVILYILLCGVPPFWAETEGQVAAILRGVLDPKRDPWPNVSENADLV 297

Qy 247 KQMLEPDSKRLTAQOVLDPHWIQNAKK 274
Db 298 RHMLEPDPKRLTAQVLEHHWLQNAKK 325

RESULT 11
US-10-425-114-65930
; Sequence 65930, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 65930
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3606-058-A10_FLI.pep
; US-10-425-114-65930

Query Match      80.1%; Score 1136; DB 15; Length 592;
Best Local Similarity 79.1%; Pred. No. 6.2e-85;
Matches 212; Conservative 26; Mismatches 30; Indels 0; Gaps 0;

Qy 7 ISDKYILGRELGRGEGFITYLCTDRETREALACKSISKRLRTAVDVEDVRREVTIMSTL 66
Db 113 IDDKYVLDRELGRGEGFITYLCTDRETREALACKSISKRLRTAVDVEDVRREVTIMSTL 172

Qy 67 PEHPNVVKLKATYEDNETVHLMELCEGGELFGRIVARGHYTERAAATVARTIAEVVRMC 126
Db 173 PKSPSVLSREACEDDGAHVLMELCEGGELFGRIVARGHYTERAAASVTRTILEVVOLC 232

Qy 127 HVGVMHRDLKPENFLFANKKENSALKAIIDFGLSVLPKPGERFTEIVGSPYYMAPEVLKR 186
Db 233 HRHGVHHRDLKPENFLFANKKENSPLKAIIDFGLSIFPKGKEFSEIVGSPYYMAPEVLKR 292

Qy 187 NYGPEVDVMSAGVILYILLCGVPPFWAETEGQVALAILRGVLDPKRDPWQISSEAKSLV 246
Db 293 NYGPEIDWSAGVILYILLCGVPPFWAETEGQVAAILRGVLDPKRDPWPNVSENADLV 352

Qy 247 KQMLEPDSKRLTAQOVLDPHWIQNAKK 274
Db 353 RHMLEPDPKRLTAQVLEHHWLQNAKK 380

RESULT 13
US-10-767-701-44784
; Sequence 44784, Application US/10767701
; Publication No. US20040172684A1

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Db 113 IDDKYVLDRELGRGEGFITYLCTDRETREALACKSISKRLRTAVDVEDVRREVTIMSTL 172
Qy 67 PEHPNVVKLKATYEDNETVHLMELCEGGELFGRIVARGHYTERAAATVARTIAEVVRMC 126
Db 173 PKSPSVLSREACEDDGAHVLMELCEGGELFGRIVARGHYTERAAASVTRTILEVVOLC 232
Qy 127 HVGVMHRDLKPENFLFANKKENSALKAIIDFGLSVLPKPGERFTEIVGSPYYMAPEVLKR 186
Db 233 HRHGVHHRDLKPENFLFANKKENSPLKAIIDFGLSIFPKGKEFSEIVGSPYYMAPEVLKR 292
Qy 187 NYGPEVDVMSAGVILYILLCGVPPFWAETEGQVALAILRGVLDPKRDPWQISSEAKSLV 246
Db 293 NYGPEIDWSAGVILYILLCGVPPFWAETEGQVAAILRGVLDPKRDPWPNVSENADLV 352
Qy 247 KQMLEPDSKRLTAQOVLDPHWIQNAKK 274
Db 353 RHMLEPDPKRLTAQVLEHHWLQNAKK 380

RESULT 12
US-10-425-114-70054
; Sequence 70054, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 70054
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMOL1719A04_FLI.pep
; US-10-425-114-70054

Query Match      80.1%; Score 1136; DB 15; Length 592;
Best Local Similarity 79.1%; Pred. No. 6.2e-85;
Matches 212; Conservative 26; Mismatches 30; Indels 0; Gaps 0;

Qy 7 ISDKYILGRELGRGEGFITYLCTDRETREALACKSISKRLRTAVDVEDVRREVTIMSTL 66
Db 113 IDDKYVLDRELGRGEGFITYLCTDRETREALACKSISKRLRTAVDVEDVRREVTIMSTL 172

Qy 67 PEHPNVVKLKATYEDNETVHLMELCEGGELFGRIVARGHYTERAAATVARTIAEVVRMC 126
Db 173 PKSPSVLSREACEDDGAHVLMELCEGGELFGRIVARGHYTERAAASVTRTILEVVOLC 232

Qy 127 HVGVMHRDLKPENFLFANKKENSALKAIIDFGLSVLPKPGERFTEIVGSPYYMAPEVLKR 186
Db 233 HRHGVHHRDLKPENFLFANKKENSPLKAIIDFGLSIFPKGKEFSEIVGSPYYMAPEVLKR 292

Qy 187 NYGPEVDVMSAGVILYILLCGVPPFWAETEGQVALAILRGVLDPKRDPWQISSEAKSLV 246
Db 293 NYGPEIDWSAGVILYILLCGVPPFWAETEGQVAAILRGVLDPKRDPWPNVSENADLV 352
Qy 247 KQMLEPDSKRLTAQOVLDPHWIQNAKK 274
Db 353 RHMLEPDPKRLTAQVLEHHWLQNAKK 380

RESULT 13
US-10-767-701-44784
; Sequence 44784, Application US/10767701
; Publication No. US20040172684A1

```

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; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 44784
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C5983_1.pep
US-10-767-701-44784

Query Match      80.0%; Score 1135; DB 16; Length 425;
Best Local Similarity 78.7%; Pred. No. 5.1e-85;
Matches 211; Conservative 26; Mismatches 31; Indels 0; Gaps 0;

QY 7 ISDKYILGRELGRGFGITYLCTDRETREALACKSISKRLRTAVDVEDVRREVIMSTL 66
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 67 IDDKYALDRELGRGFGVTYLCMDRDTKELLACKSISKRLRTAVDVEDVRREVALMRHL 132
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 67 PEHPNVVVKLKYATEDNETVHLVMECEGGEFGRIIVARGHYTERAAATVARTIAEVVVMC 126
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 133 PKASIVSLREACEDEGAHVLVMECEGGEFGELFDRIIVARGHYTERAAANVTRTIVEVQVLC 192
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 127 HVGVMHRLDKPENFLFANKKENSALKAIIDFGLSVLPKGERFTEIVGSPYYMAPEVLKR 186
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 193 HRHGVTHRLDKPENFLFANKKENSPLKAIIDFGLSIFPKGEKFSIIVGSPYYMAPEVLKR 252
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 187 NYGPEVDVMSAGVILYLLCGVPPFWAETEQGVALAILRGVLDPKRDPWSQISSEAKSLV 246
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 253 NYGPEIDVMSAGVILYLLCGVPPFWAETEQGVAAILRGVLDPKRDPWPNVSENADLV 312
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 247 KQMLEPDPKRLTAQOVLDPHPIQNAKK 274
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 313 RRMLEPDPKRLTAQVLEHPWLQNAKK 340
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 15
US-10-437-963-163957
; Sequence 163957, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 163957
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_62904C.1.pep
US-10-437-963-163957

Query Match      78.6%; Score 1115; DB 16; Length 661;
Best Local Similarity 78.1%; Pred. No. 3.8e-83;
Matches 207; Conservative 27; Mismatches 31; Indels 0; Gaps 0;

QY 10 KYILGRELGRGFGITYLCTDRETREALACKSISKRLRTAVDVEDVRREVIMSTLPEH 69
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 RYELGELGRGFGITYLCTEATGDRYACKSISKRLRTAVDVEDVRREVEIMRHPMSH 122
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 70 PNVVVKLKYATEDNETVHLVMECEGGEFGRIIVARGHYTERAAATVARTIAEVVVMCHVN 129
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 123 PNVLSRAAYEDEDNVHLVMECEGGEFGELFDRIIVARGHYTERAAANVTRTIVEVQVCHRH 182
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 130 GVMHRLDKPENFLFANKKENSALKAIIDFGLSVLPKGERFTEIVGSPYYMAPEVLKRNKG 189
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 183 GVMHRLDKPENFLYANKKSSPLKAIIDFGLSVFPFRGERFTEIVGSPYYMAPEVLKRYG 242
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 190 PEVDVMSAGVILYLLCGVPPFWAETEQGVALAILRGVLDPKRDPWSQISSEAKSLVKQM 249
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 243 PEVDVMSAGVILYLLCGVPPFWAETEQGVAQAIIRSVVDPKREPWPVSEPAKDLVKRM 302
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 250 LEPDSTKRLTAQOVLDPHPIQNAKK 274
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 303 LOPNPMTRLTAQVLEHPWLHDSKK 327
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 44784
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C5983_1.pep
US-10-767-701-44784

Query Match      80.0%; Score 1135; DB 16; Length 425;
Best Local Similarity 78.7%; Pred. No. 5.1e-85;
Matches 211; Conservative 26; Mismatches 31; Indels 0; Gaps 0;

QY 7 ISDKYILGRELGRGFGITYLCTDRETREALACKSISKRLRTAVDVEDVRREVIMSTL 66
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 67 IDDKYALDRELGRGFGVTYLCMDRDTKELLACKSISKRLRTAVDVEDVRREVALMRHL 126
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 67 PEHPNVVVKLKYATEDNETVHLVMECEGGEFGRIIVARGHYTERAAATVARTIAEVVVMC 126
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 127 PKSPSIVSLREACEDEGAHVLVMECEGGEFGELFDRIIVARGHYTERAAANVTRTIVEVQVLC 186
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 127 HVGVMHRLDKPENFLFANKKENSALKAIIDFGLSVLPKGERFTEIVGSPYYMAPEVLKR 186
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 187 HRHGVTHRLDKPENFLFANKKENSPLKAIIDFGLSIFPKGEKFSIIVGSPYYMAPEVLKR 246
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 187 NYGPEVDVMSAGVILYLLCGVPPFWAETEQGVALAILRGVLDPKRDPWSQISSEAKSLV 246
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 247 NYGPEIDVMSAGVILYLLCGVPPFWAETEQGVAAILRGVLDPKRDPWPNVSENADLV 306
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 247 KQMLEPDPKRLTAQOVLDPHPIQNAKK 274
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 307 RRMLEPDPKRLTAQVLEHHWLQNAKK 334
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 14
US-10-437-963-160820
; Sequence 160820, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 160820
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_60062C.1.pep
US-10-437-963-160820

Query Match      79.8%; Score 1132; DB 16; Length 599;
Best Local Similarity 78.7%; Pred. No. 1.3e-84;
Matches 211; Conservative 25; Mismatches 32; Indels 0; Gaps 0;

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Search completed: October 14, 2005, 11:02:47
Job time : 167 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 14, 2005, 10:58:37 ; Search time 40 Seconds

(without alignments)
659,085 Million cell updates/sec

Title: US-08-989-881-2

Perfect score: 1419

Sequence: 1 MANQTQISDKYILGRELGRG.....TKRLTAQQVLDHPWIONAKK 274

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1395	98.3	541	2	F96776	hypothetical prote
2	1322	93.2	545	2	H86322	calcium-dependent
3	1318	92.9	493	1	S46283	calcium-dependent
4	1161	81.8	560	2	T46189	calcium-dependent
5	1135	80.0	503	2	T51156	calcium-dependent
6	1127	79.4	530	2	A84847	probable Ca2+ depe
7	1127	79.4	533	1	S71778	calcium-dependent
8	1030	72.6	582	2	E84721	probable calcium-d
9	926	65.3	639	1	T02784	calcium-dependent
10	916	64.6	610	1	A49082	calcium-dependent
11	906	63.8	554	1	T03263	calcium-dependent
12	905.5	63.8	451	2	S56717	calcium-dependent
13	899	63.4	573	2	T03940	calcium-dependent
14	898	63.3	492	1	T03271	calcium-dependent
15	894.5	63.0	490	1	S71776	calcium-dependent
16	894	63.0	487	1	S71770	calcium-dependent
17	893	62.9	533	1	S56652	calcium-dependent
18	887	62.5	495	1	S46284	calcium-dependent
19	887	62.5	529	1	S71774	calcium-dependent
20	887	62.5	531	1	T02993	calcium-dependent
21	877.5	61.8	553	1	T02139	calcium-dependent
22	877	61.8	583	2	H84810	probable calcium-d
23	876	61.7	544	2	D84550	probable calmoduli
24	875	61.7	520	2	C84774	probable calcium-d
25	874	61.6	556	2	T06126	calcium-dependent
26	872	61.5	542	1	S56651	calcium-dependent
27	871	61.4	465	1	T03024	calcium-dependent
28	871	61.4	514	2	T10938	calcium-dependent
29	867	61.1	531	2	D85059	probable calcium d

30	866	61.0	520	2	F85059	probable calcium d
31	866	61.0	538	2	T08874	calcium-dependent
32	865	61.0	501	2	G85097	hypothetical prote
33	864	60.9	513	1	T02259	calcium-dependent
34	863	60.8	540	1	T01989	calcium-dependent
35	862	60.7	521	2	G96543	calcium-dependent
36	861.5	60.7	508	1	A43713	calcium-dependent
37	861	60.7	532	2	T14335	protein kinase, ca
38	857	60.4	490	2	T08873	calcium-dependent
39	854	60.2	484	2	T05650	calcium-dependent
40	850	59.9	554	2	T05476	calcium-dependent
41	822	57.9	534	1	JC1515	calcium-dependent
42	777	54.8	425	2	S17759	protein kinase, ca
43	744	52.4	571	2	T00835	calcium-dependent
44	737	51.9	591	2	S54788	calcium-stimulated
45	709	50.0	601	2	T46084	CDPK-related prote

ALIGNMENTS

RESULT 1

F96776

hypothetical protein F25A4.29 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: F96776

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alons

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maity, R.; Marzai,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:1130712

A:Accession: F96776

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-541 <STO>

A:Cross-references: UNIPROT:Q9SSF8; GB:AE005173; NID:G5882721; PIDN:AAD55274.1; GSPDB:

C:Genetics:

A:Gene: F25A4.29

A:Map position: 1

C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein k

C:Keywords: EF hand

Query Match 98.3%; Score 1395; DB 2; Length 541;
Best Local Similarity 98.2%; Pred. No. 4.8e-61;
Matches 269; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy	1	MANQTQISDKYILGRELGRGFGITYLCTDRETREALACKSISKRLRTAVDVEDVRREV	60
Db	49	MSHQSQISDKYILGRELGRGFGITYLCTDRETREALACKSISKRLRTAVDVEDVRREV	108
Qy	61	TIMSTLPHPNVKLVKATYEDNETVHLVNLCEGELFGRIVARGHYTERAAATVARTTA	120
Db	109	TIMSTLPHPNVKLVKATYEDNETVHLVNLCEGELFGRIVARGHYTERAAATVARTTA	168
Qy	121	EVVRMCHVGMHRLKPELNFANKKNSALKALDFGLSVLFKPGERFTEVGSPPYMA	180
Db	169	EVVRMCHVGMHRLKPELNFANKKNSALKALDFGLSVLFKPGERFTEVGSPPYMA	228
Qy	181	PEVLKRNYPGEVDVMSAGVILYLLCGVPPFPAETEQGVVALAILRGVLDFKRDPSQSISE	240
Db	229	PEVLKRNYPGEVDVMSAGVILYLLCGVPPFPAETEQGVVALAILRGVLDFKRDPSQSISE	288
Qy	241	SAKSLVKOMLEPDSSTKRLTAQQVLDHPWIONAKK	274
Db	289	SAKSLVKOMLEPDSSTKRLTAQQVLDHPWIONAKK	322

RESULT 2
H86322
calcium-dependent protein kinase 1 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: H86322
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: H86322
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-545 <STO>
A;Cross-references: UNIPROT:Q9M9V8; GB:AE005172; NID:g6730697; PIDN:AAF27092.1; GSPDB:GN
C;Genetics:
A;Map position: 1
C;Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin
C;Keywords: EF hand

Query Match 93.2%; Score 1322; DB 2; Length 545;
Best Local Similarity 92.3%; Pred. No. 1.6e-57;
Matches 253; Conservative 8; Mismatches 13; Indels 0; Gaps 0;
Qy 1 MANQTQISDKYILGRELGRGFGITLYCTDRETRALACKSISKRKLRTAVDVEDVRREV 60
Db 53 MSNQTQISDKYILGRELGRGFGITLYCTDRETRALACKSISKRKLRTAVDIEDVRREV 112
Qy 61 TIMSTLPEHPNVVKLKATYEDNETVHLMELCEGELFGRIVARGHYTERAAATVARTIA 120
Db 113 AIMSTLPEHPNVVKLKASYEDNENHLMELCEGELFDRIVARGHYTERAAAAVARTIA 172
Qy 121 EVVRMCHVNGVMHRDLKPENFLFANKKENSALKDAIDFGLSVLPKPGGRFTEIVGSPYMA 180
Db 173 EVVMCHSNGVMHRDLKPENFLFANKKENSPLKDAIDFGLSVFPKPGDKFTEIVGSPYMA 232
Qy 181 PEVLKRNYPGEVDVWSAGVILYILLCGVPFPAETEQGVVALAILRGVLDKFRDWPQISE 240
Db 233 PEVLKRDYGPVDVWSAGVILYILLCGVPFPAETEQGVVALAILRGVLDKFRDWPQISE 292
Qy 241 SAKSLVKQMLPDPSTKRLTAQOVLDPHPIQNAKK 274
Db 293 SAKSLVKQMLPDPSTKRLTAQOVLDPHPIQNAKK 326

RESULT 3
S46283
calcium-dependent protein kinase (EC 2.7.1.1) - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C;Accession: S46283
R;Urao, T.; Katagiri, T.; Mizoguchi, T.; Yamaguchi-Shinozaki, K.; Hayashida, N.; Shinoza
Mol. Gen. Genet. 244, 331-340, 1994
A;Title: Two genes that encode Ca(2+)-dependent protein kinases are induced by drought a
A;Reference number: S46283; MUID:943359455; PMID:8078458
A;Accession: S46283
A;Molecule type: mRNA
A;Residues: 1-493 <URA>
A;Cross-references: UNIPROT:Q39015; EMBL:D21805; NID:g1235716; PIDN:BAA04829.1; PID:g604
C;Genetics:
A;Gene: CDPK1
C;Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin
C;Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific
F;9-269/Domain: protein kinase homology <KIN>
F;17-25/Region: protein kinase ATP-binding motif

F;312-344/Domain: calmodulin repeat homology <EF1>
F;348-380/Domain: calmodulin repeat homology <EF2>
F;384-416/Domain: calmodulin repeat homology <EF3>
F;420-452/Domain: calmodulin repeat homology <EF4>
F;40/Active site: Lys #status predicted

Query Match 92.9%; Score 1318; DB 1; Length 493;
Best Local Similarity 92.0%; Pred. No. 2.4e-57;
Matches 252; Conservative 8; Mismatches 14; Indels 0; Gaps 0;
Qy 1 MANQTQISDKYILGRELGRGFGITLYCTDRETRALACKSISKRKLRTAVDVEDVRREV 60
Db 1 MSNQTQISDKYILGRELGRGFGITLYCTDRETRALACKSISKRKLRTAVDIEDVRREV 60
Qy 61 TIMSTLPEHPNVVKLKATYEDNETVHLMELCEGELFGRIVARGHYTERAAATVARTIA 120
Db 61 AIMSTLPEHPNVVKLKASYEDNENHLMELCEGELFDRIVARGHYTERAAAAVARTIA 120
Qy 121 EVVRMCHVNGVMHRDLKPENFLFANKKENSALKDAIDFGLSVLPKPGGRFTEIVGSPYMA 180
Db 121 EVVMCHSNGVMHRDLKPENFLFANKKENSPLKDAIDFGLSVFPKPGDKFTEIVGSPYMA 180
Qy 181 PEVLKRNYPGEVDVWSAGVILYILLCGVPFPAETEQGVVALAILRGVLDKFRDWPQISE 240
Db 181 PEVLKRDYGPVDVWSAGVILYILLCGVPFPAETEQGVVALAILRGVLDKFRDWPQISE 240
Qy 241 SAKSLVKQMLPDPSTKRLTAQOVLDPHPIQNAKK 274
Db 241 SAKSLVKQMLPDPSTKRLTAQOVLDPHPIQNAKK 274

RESULT 4

T46189
calcium-dependent protein kinase - Arabidopsis thaliana
N;Alternate names: protein T8H10.130
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T46189
R;Benes, V.; Rechmann, S.; Borkova, D.; Ansoorge, W.; Mewes, H.W.; Lemcke, K.; Mayer, K.
submitted to the Protein Sequence Database, January 2000
A;Reference number: 223014
A;Accession: T46189
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-560 <BEN>
A;Cross-references: UNIPROT:Q9SCMO; EMBL:AL133248
A;Experimental source: cultivar Columbia; BAC clone T8H10
C;Genetics:
A;Map position: 3
A;Introns: 176/3; 218/1; 266/1; 317/1; 355/3; 411/3; 487/3; 532/3
A;Note: T8H10.130
C;Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein ki
C;Keywords: EF hand

Query Match 81.8%; Score 1161; DB 2; Length 560;
Best Local Similarity 79.5%; Pred. No. 1.1e-49;
Matches 213; Conservative 24; Mismatches 31; Indels 0; Gaps 0;
Qy 6 QISDKYILGRELGRGFGITLYCTDRETRALACKSISKRKLRTAVDVEDVRREVIMST 65
Db 58 EIESKYTLGRELGRGFGITLYCTDRETRALACKSISKRKLRTAVDIEDVRREVIMRH 117
Qy 66 LPEHPNVVKLKATYEDNETVHLMELCEGELFGRIVARGHYTERAAATVARTIAEVVRM 125
Db 118 MPEHPNVVTLKETYEDEHVAHLMELCEGELFDRIVARGHYTERAAAAVTIMEVQV 177
Qy 126 CHVNGVMHRDLKPENFLFANKKENSALKDAIDFGLSVLPKPGGRFTEIVGSPYMAPEVLK 185
Db 178 CHVNGVMHRDLKPENFLFANKKENSALKDAIDFGLSVFPKPGDKFTEIVGSPYMAPEVLK 237
Qy 186 RNYGPEVDVWSAGVILYILLCGVPFPAETEQGVVALAILRGVLDKFRDWPQISEAKSL 245
Db 238 RNYGPEVDVWSAGVILYILLCGVPFPAETEQGVVALAILRGVLDKFRDWPQISEAKSL 297

QY 246 VKOMLEPDSTKRLTAQVLDHPWIONAK 273
DB 298 IRKMLDPDQKRRLTAQVLDHPWIONAK 325

RESULT 5

T51156
calcium dependent protein kinase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 09-Jul-2004
C:Accession: T51156
R:Comella, P.; Wu, H.J.; Laudie, M.; Berger, C.; Cooke, R.; Delseeny, M.; Grelllet, F.
Plant Mol. Biol. 41, 687-700, 1999
A:Title: Fine sequence analysis of 60 kb around the Arabidopsis thaliana AtEm1 locus on
A:Reference number: 224835; MUID:20108326; PMID:10645728
A:Accession: T51156
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-503 <COM>
A:Cross-references: UNIPROT:Q96294; EMBL:AF049236; PIDN:AAC14412.1
R:Grelllet, F.; Wu, H.J.; Gaubier-Comella, P.; Berger, C.; Mares, G.; Delseeny, M.
submitted to the EMBL Data Library, March 1996
A:Description: A new member of the calcium-dependent protein kinase gene family in Arabi
A:Reference number: 225320
A:Accession: T51165
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-503 <GRE>
A:Cross-references: EMBL:U54615; PIDN:AAA99794.1
A:Experimental source: Cultivar Columbia
C:Genetics:
A:Map position: 3
A:Introns: 209/1; 257/1; 308/3; 346/3; 402/3; 425/3; 454/3
C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin
C:Keywords: EF hand

Query Match 80.0%; Score 1135; DB 2; Length 503;
Best Local Similarity 78.0%; Pred. No. 1.8e-48;
Matches 209; Conservative 31; Mismatches 28; Indels 0; Gaps 0;

QY 7 ISDKYILGRELGRGEFGITVLCYDRETRALACKSISKRLTAVDVEDVRREVTIMSTL 66
DB 50 IEDRYLLDRELGRGEFGVYLCIERSRDLACKSISKRLTAVDIEDVKREIVAKML 109
QY 67 PEHPNVVKLKYATEDNETVHLMVLCGEGELFGRIVARGHYTERAAATVARTIAEVVRC 126
DB 110 PKSSIVTLKEACEDDNAVHLMVLCGEGELFGRIVARGHYTERAAAGVTKTIVEVVQLC 169
QY 127 HNGVMHRDLKPNFLFANKKENSALKKIDFGLSVLFKPGERTFIVGSPYYMAPEVLKR 186
DB 170 HKHGVTHRDLKPNFLFANKKENSPLKIDFGLSIFPKGKFESEIVGSPYYMAPEVLKR 229
QY 187 NYGPEVDVMSAGVILYLLCGVPPFWAETEQGVVALAILRGVLDPKRDPMSQISESAKSLV 246
DB 230 NYGPEIDVMSAGVILYLLCGVPPFWAETEQGVVALAILRGVLDPKRDPMSQISESAKSLV 299
QY 247 KQMLEPDSTKRLTAQVLDHPWIONAK 274
DB 290 RQMLEPDSTKRLTAQVLDHPWIONAK 317

RESULT 6

A84847
probable Ca2+ dependent protein kinase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: A84847
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: A84847
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-530 <STO>

A:Cross-references: UNIPROT:P93759; GB:AE002093; NID:g1871195; PIDN:AA63555.1; GSPDB

C:Genetics:

A:Gene: At2g41860

A:Map position: 2

C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein

C:Keywords: EF hand

Query Match 79.4%; Score 1127; DB 2; Length 530;
Best Local Similarity 76.5%; Pred. No. 4.5e-48;
Matches 205; Conservative 32; Mismatches 31; Indels 0; Gaps 0;

QY 6 QISDKYILGRELGRGEFGITVLCYDRETRALACKSISKRLTAVDVEDVRREVTIMST 65

DB 49 EIKQYKLGRELGRGEFGVYLCIETETGEIACKSILKKLTKSIDIEDVKREIVEIMRQ 108

QY 66 LPEHPNVVKLKYATEDNETVHLMVLCGEGELFGRIVARGHYTERAAATVARTIAEVVRC 125

DB 109 MPEHPNVITLKYETEDDKAVHLMVLCGEGELFDRIVARGHYTERAAASVITLIEVVQM 168

QY 126 CHVNGVMHRDLKPNFLFANKKENSALKKIDFGLSVLFKPGERTFIVGSPYYMAPEVLK 185

DB 169 CHKHGVMHRDLKPNFLFANKKETSALKKIDFGLSVLFKPGERTFIVGSPYYMAPEVLK 228

QY 186 RNYGPEVDVMSAGVILYLLCGVPPFWAETEQGVVALAILRGVLDPKRDPMSQISESAKSL 245

DB 229 RSYGQIEDVMSAGVILYLLCGVPPFWAETEHGVAIKLSVIDFKRDPMPKVSNDNAKDL 288

QY 246 VKOMLEPDSTKRLTAQVLDHPWIONAK 273

DB 289 IKKMLHPDPRRLTAQVLDHPWIONAK 316

RESULT 7

S71778
calcium-dependent protein kinase (EC 2.7.1.-) 19 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004

C:Accession: S71777; S71198

R:Hong, Y.; Takano, M.; Liu, C.M.; Gasch, A.; Chye, M.L.; Chua, N.H.

Plant Mol. Biol. 30, 1259-1275, 1996

A:Title: Expression of three members of the calcium-dependent protein kinase gene fami

A:Reference number: S71774; MUID:96311013; PMID:8704134

A:Accession: S71778

A:Molecule type: DNA

A:Residues: 1-533 <HON>

A:Cross-references: UNIPROT:Q42438; EMBL:U20627; NID:g836947; PIDN:AAA67658.1; PID:g83

A:Accession: S71777

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 56-533 <HOW>

A:Cross-references: EMBL:U20624

C:Genetics:

A:Gene: CDPKL9

A:Introns: 170/3; 211/1; 260/1; 311/1; 349/3; 406/3; 483/3

C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein

C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specif

F:55-315/Domain: protein kinase homology <KIN>

F:63-71/Region: protein kinase ATP-binding motif

F:358-390/Domain: calmodulin repeat homology <EF1>

F:395-427/Domain: calmodulin repeat homology <EF2>

F:431-463/Domain: calmodulin repeat homology <EF3>

F:467-499/Domain: calmodulin repeat homology <EF4>

F:86/Active site: Lys #status predicted

Query Match 79.4%; Score 1127; DB 1; Length 533;
Best Local Similarity 78.7%; Pred. No. 4.5e-48;
Matches 211; Conservative 25; Mismatches 32; Indels 0; Gaps 0;

A:Gene: CPK1
A:Function:
A:Description: serine/threonine-specific protein kinase activated by direct binding of
C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin
C:Keywords: ATP; calcium binding; EF hand; membrane protein; myristylation; phosphotrans
F:108-368/Domain: protein kinase homology <KIN>
F:447-479/Domain: calmodulin repeat homology <EFH>

Query Match 63.4%; Score 899; DB 2; Length 573;
Best Local Similarity 63.5%; Pred. No. 5.3e-37;
Matches 165; Conservative 35; Mismatches 60; Indels 0; Gaps 0;

Qy 11 YILGRELGRGPGITVLTCTDRETRALACKSISKRLTAVDVEDVREVTIMSTLPHP 70
Db 110 YSLGKLGQGGPGITVLTCTDRETRALACKSISKRLTAVDVEDVREVTIMSTLPHP 169
Qy 71 NVVVKATYEDNETVHLMVCEGELGRIIVARGHYTERAAATVARTIAEVVRCHVNG 130
Db 170 NVISIKGAYEDAVAVQVMELCAGGELFDRIIQRGHYTERKAAELTRIIVGVLEACHALG 229
Qy 131 VMHRLDKPENFLFANKKENSALKADIFGLSVLFKPGERFTEIVGSPYYMAPEVLKRYGP 190
Db 230 VMHRLDKPENFLFVSKESLKTIDFGLSMFPGKGFNDVVGSPYYVAPEVLKRYGP 289
Qy 191 EVDVMSAGVILYILCGVPPFPAETEGVALAILRGVLDKEDPKSQISSESAKSLAVKWL 250
Db 290 EADVMSAGVIVYILSGVPPFPAESEGEFIEVLHGLDLDFFSDPWPISDSAKDLVRRML 349
Qy 251 EPDSTKRLTAQOVLDPHWIQ 270
Db 350 VRDPRKRLTAPEVLCHPWVQ 369

RESULT 14
T03271
calcium-dependent protein kinase (EC 2.7.1.1) 1 - maize
C:Species: Zea mays (maize)
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C:Accession: T03271
R:Berberich, T.; Kusano, T.
Mol. Gen. Genet. 254, 275-283, 1996
A:Title: Cycloheximide induces a subset of low temperature-inducible genes in maize.
A:Reference number: Z14873
A:Accession: T03271
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-492 <BER>
A:Cross-references: UNIPROT:Q04417; EMBL:D84408; PIDN:BAA12338.1
A:Experimental source: strain honey bantum
A:Note: low temperature-inducible
C:Genetics:
A:Gene: CDPK1
C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin
C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific
F:25-285/Domain: protein kinase homology <KIN>
F:33-41/Region: protein kinase ATP-binding motif
F:328-360/Domain: calmodulin repeat homology <EF1>
F:364-396/Domain: calmodulin repeat homology <EF2>
F:400-432/Domain: calmodulin repeat homology <EF3>
F:434-466/Domain: calmodulin repeat homology <EF4>
F:56/Active site: Lys #status predicted

Query Match 63.3%; Score 898; DB 1; Length 492;
Best Local Similarity 63.4%; Pred. No. 5.2e-37;
Matches 168; Conservative 36; Mismatches 61; Indels 0; Gaps 0;

Qy 7 ISDKYILGRELGRGFGITVLTCTDRETRALACKSISKRLTAVDVEDVREVTIMSTL 66
Db 23 LRDLVALGRKGGGFGITVLTCTELATGIDYACKSISKRLTKEDVDVREIQTIMHLL 82
Qy 67 PPHNPVVKATYEDNETVHLMVCEGELGRIIVARGHYTERAAATVARTIAEVVRMC 126
Db 83 SGHKNVVAIKGAYEDQVYVHVMELCAGELFDRIIQRGHYTERKAAALTRIIVGVVEAC 142

Qy 127 HVGVMHRLDKPENFLFANKKENSALKADIFGLSVLFKPGERFTEIVGSPYYMAPEVLKR 186
Db 143 HSLGVMHRLDKPENFLANRDDDLSLKAIDFGLSVFVKPGQVFTDVVGSPYYVAPEVLK 202
Qy 187 NYGPEVDVMSAGVILYILCGVPPFPAETEGVALAILRGVLDKEDPKRDPWSOISSESAKSLV 246
Db 203 SYGPAADVWTAGVILYILSGVPPFPAETQGIQIDAVLKGAIIDFSDPWPVSDSAKDLI 262
Qy 247 KOMLEPSTKRLTAQOVLDPHWIQ 271
Db 263 RRMLNPRPAERLTAHEVLCHPWIRD 287

RESULT 15
S71776

calcium-dependent protein kinase (EC 2.7.1.1) 9 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C:Accession: S71776; S71775; S71902; S71196
R:Hong, Y.; Takano, M.; Liu, C.M.; Gasch, A.; Chye, M.L.; Chua, N.H.
Plant Mol. Biol. 30, 1259-1275, 1996
A:Title: Expression of three members of the calcium-dependent protein kinase gene fami
A:Reference number: S71774; MUID:96311013; PMID:8704134

A:Accession: S71776
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-490 <HON>
A:Cross-references: UNIPROT:Q42396; EMBL:U20626
A:Accession: S71775
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-490 <HOP>
A:Cross-references: EMBL:U20388
R:Hong, Y.; Takano, M.; Liu, C.M.; Gasch, A.; Chye, M.L.; Tan, C.T.; Koh, C.C.; Chua, N.
submitted to the EMBL Data Library, February 1995
A:Description: Expression of the calcium-dependent protein kinase gene family in Arabi
A:Reference number: S71197
A:Accession: S71902
A:Molecule type: DNA
A:Residues: 1-164, 'S', 166-239, 'E', 241-300, 'KF', 303-350, 'S', 352-490 <HOW>
A:Cross-references: EMBL:U20626; NID:9836945; PIDN:AAA67657.1; PID:9836946
R:Hong, Y.; Takano, M.; Liu, C.M.; Gasch, A.; Chye, M.L.; Tan, C.T.; Koh, C.C.; Chua, N.
submitted to the EMBL Data Library, January 1995
A:Description: Expression of the calcium dependent protein kinase gene family in Arabi
A:Reference number: S71196
A:Accession: S71196
A:Molecule type: mRNA
A:Residues: 1-164, 'S', 166-239, 'E', 241-300, 'KF', 303-350, 'S', 352-490 <HOA>
A:Cross-references: EMBL:U20388; NID:9836937; PIDN:AAA67653.1; PID:9836938
C:Genetics:
A:Gene: CDPK9
A:Introns: 177/1; 225/1; 276/1; 370/3; 445/3
C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein k
C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specif
F:20-280/Domain: protein kinase homology <KIN>
F:28-36/Region: protein kinase ATP-binding motif
F:323-355/Domain: calmodulin repeat homology <EF1>
F:352-391/Domain: calmodulin repeat homology <EF2>
F:395-427/Domain: calmodulin repeat homology <EF3>
F:429-461/Domain: calmodulin repeat homology <EF4>
F:51/Active site: Lys #status predicted

Query Match 63.0%; Score 894.5; DB 1; Length 490;
Best Local Similarity 60.2%; Pred. No. 7.6e-37;
Matches 171; Conservative 41; Mismatches 61; Indels 11; Gaps 1;

Qy 1 MANOTQ-----ISDKYILGRELGRGFGITVLTCTDRETRALACKSISKRLKRT 49
Db 1 MANPRTRVLPYTKKVEDNYFLGVLGQQGFTTFLCTHKQTGQKLACKSIPKRLJC 60
Qy 50 ADVVEDVRREVTIMSTLPEHNPVVKLKYATYEDNETVHLMVCEGELGRIIVARGHYTE 109

```

Db      61 QEDYDDVLRREIQIMHHLSEYPNVVRIESAYEDTKNVHVMELCEGGELFDRIVKRGHYSE 120
Qy      110 RAAATVARTIAEVVRMCHVNGVHRDLKPENFLPANKKENSALKAIIDFGLSVLFKPCGERF 169
Db      121 REAAKLIKTIIVGVVEACHSLGVVHRDLKPENFLFSSSDEDEASLKATDFGLSVFCTPGEAF 180
Qy      170 TEIVGSPYNAPEVLKKNYGPEDVMSAGVILYLLCGVPPFWAETEOGVVALAILRGVLD 229
Db      181 SELVGSAYYVAPVHLKHGYPEDVMSAGVILYLLCGVPPFWAETEOGVVALAILRGVLD 240
Qy      230 FKRDPMWSQISESAKSLVKOMLEPDSTKRLTAQQVLDHPWIONAK 273
Db      241 FEINPMPSISESAKDLIKKMLESNPKKRLTAHQVLCHPWIVDDK 284

```

Search completed: October 14, 2005, 11:09:27
 Job time : 41 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 10:54:56 ; Search time 176 Seconds
(without alignments)
797.214 Million cell updates/sec

Title: US-08-989-881-2

Perfect score: 1419

Sequence: 1 MANQTOISDKVILGRELGRG.....TKRLTAQVLDHPWQNAKK 274

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	1419	100.0	274	Q9SB23	Q9sb23 arabidopsis
2	1395	98.3	541	Q9SFP8	Q9sf8 arabidopsis
3	1322	93.2	545	Q9M9V8	Q9m9v8 arabidopsis
4	1318	92.9	493	Q39015	Q39015 arabidopsis
5	1318	92.9	545	Q84W07	Q84w07 arabidopsis
6	1186	83.6	518	Q94952	Q94952 funaria hyg
7	1161	81.8	538	Q6NLQ6	Q6nlq6 arabidopsis
8	1161	81.8	560	Q9SGM0	Q9sgm0 arabidopsis
9	1158	81.6	529	Q48565	Q48565 fragaria an
10	1155	81.4	550	Q84SL0	Q84sl0 oryza sativ
11	1142	80.5	528	Q6KCS4	Q6kcs4 nicotiana p
12	1141	80.4	522	Q8H1T8	Q8h1t8 ceratopteris
13	1141	80.4	535	Q38873	Q38873 arabidopsis
14	1135	80.0	503	Q96294	Q96294 arabidopsis
15	1135	80.0	528	Q8W4I7	Q8w4i7 arabidopsis
16	1132	79.8	531	Q8LKEZ7	Q8lke7 oryza sativ
17	1127	79.4	530	Q93759	Q93759 arabidopsis
18	1127	79.4	533	Q42438	Q42438 arabidopsis
19	1115	78.6	538	Q75G88	Q75g88 oryza sativ
20	1106	77.9	547	Q6I5I8	Q6i5i8 oryza sativ
21	1094	77.1	574	Q6AVI8	Q6avi8 oryza sativ
22	1030	72.6	582	Q8G375	Q8g375 arabidopsis
23	1030	72.6	582	Q9SIQ7	Q9siq7 arabidopsis
24	957	67.4	548	Q9S786	Q9s786 marchantia
25	957	67.4	548	Q9S724	Q9s724 marchantia
26	932	65.7	599	Q6F3A6	Q6f3a6 oryza sativ
27	930	65.5	528	Q8VYE7	Q8vye7 arabidopsis
28	929.5	65.5	577	Q69IM9	Q69im9 oryza sativ
29	929	65.3	528	Q9FMPS	Q9fmps arabidopsis
30	926	65.3	639	O82107	O82107 zea mays (m
31	919	64.8	646	Q38870	Q38870 arabidopsis

RESULT 1

ID	Q9SB23	PRELIMINARY;	PRT;	274 AA.
AC	Q9SB23;			
DT	01-MAY-2000 (Tremblrel. 13, Created)			
DT	01-MAY-2000 (Tremblrel. 13, Last sequence update)			
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)			
DE	AtCDPK1a (Fragment).			
GN	Name=cpk1a;			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; rosids;			
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsi.			
OX	NCBI_TaxID=3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Sheen J.;			
RL	Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.			
CC	-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.			
DR	EMBL; U73610; AAF14337.1; -.			
DR	HSSP; P49137; INXK.			
DR	GO; GO:0005524; F:ATP binding; IEA.			
DR	GO; GO:0016740; F:protein serine/threonine kinase activity; IEA.			
DR	GO; GO:0006468; F:protein amino acid phosphorylation; IEA.			
DR	InterPro; IPR011009; Kinase_like.			
DR	InterPro; IPR00719; Prot_kinase.			
DR	InterPro; IPR002290; Ser_thr_pkinase.			
DR	Pfam; PF00069; Pkinase; I.			
DR	ProDom; PD000001; Prot_kinase; 1.			
DR	SMART; SM00220; S_TKc; 1.			
DR	PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.			
DR	PROSITE; PSS0011; PROTEIN KINASE DOM; 1.			
DR	PROSITE; PS00108; PROTEIN KINASE ST; 1.			
KW	ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.			
FT	NON_TER 274 274			
SQ	SEQUENCE 274 AA; 30909 MW; 8C6E5A1B097226ED CRC64;			

Query Match 100.0%; Score 1419; DB 2; Length 274;
Best Local Similarity 100.0%; Pred. No. 2.2e-89;
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MANQTOISDKVILGRELGRGFGITVLTCDRETREALACKSISKRKLRTAVDVEDVRREV	60
Db	1	MANQTOISDKVILGRELGRGFGITVLTCDRETREALACKSISKRKLRTAVDVEDVRREV	60
Qy	61	TTMSTLPEHPNVVVKLKATYEDNETVHLVNLCEGGLFGRIVARGHYTERAAATVARTIA	120
Db	61	TTMSTLPEHPNVVVKLKATYEDNETVHLVNLCEGGLFGRIVARGHYTERAAATVARTIA	120
Qy	121	EVRMCHVNGVMHRDLKPNFNLFPANKKENSALKAIIDFGLSVLPFKGERFTEIVGSPYYMA	180
Db	121	EVRMCHVNGVMHRDLKPNFNLFPANKKENSALKAIIDFGLSVLPFKGERFTEIVGSPYYMA	180

QY 181 PEVLKRNYPGVDSAGVILYLLCGVPPFWAETQGVVALAILRGVLDKRDPSQISE 240
 |||||
 DB 181 PEVLKRNYPGVDSAGVILYLLCGVPPFWAETQGVVALAILRGVLDKRDPSQISE 240
 |||||
 QY 241 SAKSLVKQMLEPDSKRLTAQOVLDPHPWQNAKK 274
 |||||
 DB 241 SAKSLVKQMLEPDSKRLTAQOVLDPHPWQNAKK 274
 |||||

RESULT 2
 Q9S8F8 PRELIMINARY; PRT; 541 AA.

AC Q9S8F8
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE F2S4.29 protein (Atlg74740) (Calcium-dependent protein kinase,
 putative).
 GN Name=F2S4.29; Synonyms=Atlg74740;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
 RA Lee J.M., Li J., Gonzalez A., Liu A., Liu K., Vaysberg M., Sakano H.,
 RA Chin C., Choi E., Chiou J., Altfafi H., Araujo R., Brooks S.,
 RA Buehler E., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N.,
 RA Hwang B., Huizar L., Khan S., Kim C., Palm C., Rowley D., Shinn P.,
 RA Walker M., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.,
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kim C.J., Chen H., Cheuk R., Shinn P., Bowser L., Carninci P.,
 RA Dale J.M., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,
 RA Karlin-Neumann G., Kawai J., Lam B., Lin J., Miranda M., Narusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
 RA Seki M., Southwick A., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G.,
 RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Tripp M., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
 RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
 RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
 RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
 RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
 RA Ecker J., Theologis A., Davis R.W.,
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; AC008263; AAD55274.1; -;
 DR EMBL; BT008900; AAP68339.1; -;
 DR EMBL; AY140016; AM98158.1; -;
 DR PIR; F96776; F96776.
 DR HSP; P49137; INXX.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0006468; F:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR010983; Kinase like.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR Pfam; PF00036; ehand; 4.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000012; EF-hand; 2.
 DR ProDom; PD000001; Prot_kinase; 1.

DR SMART; SM00054; EFh; 4.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS0018; EF_HAND; UNKNOWN 4.
 DR PROSITE; PS0107; PROTEIN_KINASE_ATP; UNKNOWN 1.
 DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 541 AA; 61404 MW; 7D10F76BFAFCB4C4 CRC64;

Query Match 98.3%; Score 1395; DB 2; Length 541;
 Best Local Similarity 98.2%; Pred. No. 2e-87;
 Matches 269; Conservative 3; Mismatches 0; Gaps 0;

QY 1 MANQTQSDKYILGRELGRGFGITYLCTDRETREALACKSISKRLTAVDVEVRREV 60
 |||||
 DB 49 MSHQSQISDKYILGRELGRGFGITYLCTDRETREALACKSISKRLTAVDVEVRREV 108
 |||||
 QY 61 TIMSTLPEHPNVKLKATYEDNETVHLVMECEGELFGRIVARGHYTERAAATVARTIA 120
 |||||
 DB 109 TIMSTLPEHPNVKLKATYEDNETVHLVMECEGELFGRIVARGHYTERAAATVARTIA 168
 |||||
 QY 121 EVWRMCHVNGVYHRDLKPNFLFANKKENSALKALDFGLSVLFKPGERFTEIVGSPYYNA 180
 |||||
 DB 169 EVWRMCHVNGVYHRDLKPNFLFANKKENSALKALDFGLSVLFKPGERFTEIVGSPYYNA 228
 |||||
 QY 181 PEVLKRNYPGVDSAGVILYLLCGVPPFWAETQGVVALAILRGVLDKRDPSQISE 240
 |||||
 DB 229 PEVLKRNYPGVDSAGVILYLLCGVPPFWAETQGVVALAILRGVLDKRDPSQISE 288
 |||||
 QY 241 SAKSLVKQMLEPDSKRLTAQOVLDPHPWQNAKK 274
 |||||
 DB 289 SAKSLVKQMLEPDSKRLTAQOVLDPHPWQNAKK 322
 |||||

RESULT 3
 Q9M9V8 PRELIMINARY; PRT; 545 AA.

ID Q9M9V8
 AC Q9M9V8
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Calcium-dependent protein kinase 1.
 GN Name=FA14.1;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
 RA Altfafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,
 RA Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,
 RA Lucos S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,
 RA Walker M., Yu G., Ecker J., Theologis A., Davis R.W.,
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; AC011809; AAF27092.1; -;
 DR PIR; H86322; H86322.
 DR HSP; P49137; INXX.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0006468; F:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR02048; EF-hand.
 DR InterPro; IPR010983; Kinase like.
 DR InterPro; IPR01009; Prot_kinase.
 DR InterPro; IPR000719; Ser_thr_kinase.
 DR InterPro; IPR002290; Ser_thr_pkin_AS.
 DR Pfam; PF00036; ehand; 4.
 DR Pfam; PF00069; Pkinase; 1.

DR		ProDom:	P0000012;	EF-hand; 2.
DR		ProDom:	P0000001;	Prot_kinase; 1.
DR		SMART:	SMO0054;	Efh; 4.
DR		SMART:	SMO0220;	S_TKc; 1.
DR		PROSITE:	PS00018;	EF HAND; UNKNOWN_3.
DR		PROSITE:	PS00107;	PROTEIN_KINASE_ATP; UNKNOWN_1.
DR		PROSITE:	PS00011;	PROTEIN_KINASE_DOM; 1.
DR		PROSITE:	PS00108;	PROTEIN_KINASE_ST; 1.
KW		ATP-binding:	Kinase; Serine/threonine-protein kinase;	Transferase.
SQ		SEQUENCE	545 AA;	61459-MW; A505PB320E7818E9 CRC64;

Query Match	93.2%;	Score 1322;	DB 2;	Length 545;
Best Local Similarity	92.3%;	Pred. No. 2e-82;		
Matches 253;	Conservative	8;	Mismatches 13;	Indels 0; Gaps 0;

Qy	1	MANQTQSDKYLGRGLRGEGFGITYLCTDRETRREALACKSISRRKLRTAVDVEDVREV	60
Dd	53	MSNQTQSDKYLGRGLRGEGFGITYLCTDRETHEALACKSISRKLRTAVDIEDVREV	112
Qy	61	TIMSTLEPHNPVKLTAYEDNETVHLVMELCEGELFGRIVARGHYTERAAATVARTIA	120
Dd	113	AIMSTLEPHNPVKLKASYEDNNVNHLVMELCEGELFDRIVARGHYTERAAAAVARTIA	172
Qy	121	EVPVMCHVGWHRDLPENFLFANKENSALKAIIDFGLSVLFPGGERFTIIGVSPIYMA	180
Dd	173	EVMMCHSGNVHMRDLKPENFLFANKENSPLKAIDFGLSVFFXPKDGKFTIIGVSPIYMA	232
Qy	181	PEVLKRNYGPEVDVWSAGVILYLLCGVPPPWAEIOGVALLRGLVDKFDRDPWOISE	240
Dd	233	PEVLKRYDIGPEVDVWSAGVIYYLLCGVPPPWAEIOGVALLRGLVDKFDRDPWOISE	292
Qy	241	SAKSLSVKQMLEDPTSKRLTAQQVLDHPWIQNAKK	274
Dd	293	SAKSLSVKQMLDDPTFKELTAQQVLAHPWIQNAKK	326

RESULT 4

Q39015 PRELIMINARY; PRT; 493 AA.

AC Q39015;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Calcium-dependent protein kinase.

GN Name=ATCDPK1,

OC Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosoids II; Brassicales; Brassicaceae; Arabidopsids.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=9435945; PubMed=8078458;

RA Urao T., Kagegiri T., Mizoguchi T., Yamaguchi-Shinozaki K., Hayashida N., Shinozaki K.;

RT "Two genes that encode Ca²⁺-dependent protein kinases are induced by drought and high-salt stresses in Arabidopsis thaliana.";

RL Mol. Gen. Genet. 244:331-340(1994)

CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

DR ENMBL; D21805; BAA04829.1; -.

DR PIR; S46283; S46283.

DR HSSP; P49137; INMK.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0005509; F:calcium ion binding; IEA.

DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

DR GO; GO:0016740; F:transferase activity; IEA.

DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

DR InterPro; IPR002048; EF-hand.

DR InterPro; IPR010983; EF Hand like.

DR InterPro; IPR011009; Kinase Like.

DR InterPro; IPR000719; Prot_kinase.

DR InterPro; IPR002290; Ser_thr_pkinase.

DR InterPro; IPR008271; Ser_thr_pkin AS.

DR InterPro; IPR002290; Ser thr kinase.
DR InterPro; IPR008271; Ser thr pkin_AS.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00018; EF HAND; UNKNOWN 3.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 545 AA; 61487 MW; 6957D76A1E7D93E4 CRC64;

Query Match 92.9%; Score 1318; DB 2; Length 545;
Best Local Similarity 92.0%; Pred. No. 3.8e-82;
Matches 252; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 1 MANQTOISDKYILGRELGRGEGITYLCTDRETRALACKSISKRLRTAVDVEDVRREV 60
DB 53 MSNQTQISDKYILGRELGRGEGITYLCTDRETRALACKSISKRLRTAVDIEDVRREV 112

QY 61 TIMSTLPEHPNVVVKATYEDNETVHLMELCEGELFGRIVARGHYTERAAATVARTIA 120
DB 113 AIMSTLPEHPNVVVKASYEDNENVHLMELCEGELFDRIVARGHYTERAAAAVVRTIA 172

QY 121 EYVRCHVNGVMHRLDKPENFLFANKKENSALKKIDFGLSVLPKGERFTEIVGSPYYMA 180
DB 173 EVVMCHSNGVMHRLDKPENFLFANKKENSPLKKAIDFGLSVFPKGERFTEIVGSPYYMA 232

QY 181 PEVLKRNYPGVVDVMSAGVILYLLCGVPPFWAETEQGVVALAILRGVLDKRDPMQISE 240
DB 233 PEVLKRDYGPVVDVMSAGVILYLLCGVPPFWAETEQGVVALAILRGVLDKRDPMQISE 292

QY 241 SAKSLVKOMLEPDSSTKRLTAQOVLDPHPIQNAK 274
DB 293 SAKSLVKOMLEPDPKRLTAQOVLDPHPIQNAK 326

RESULT 6
Q94G52 PRELIMINARY; PRT; 518 AA.
AC Q94G52; (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 26, Last annotation update)
DE Calcium-dependent protein kinase (Fragment).
OS Funaria hygrometrica (Moss).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Funariidae; Funariales; Funariaceae; Funaria.
OX NCBI_TaxID=29583;
RN [1] SEQUENCE FROM N.A.
RP Mitra D., Johri M.M.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AA0276999; AAF62812.1; -.
DR HSSP; P49137; 1NXX.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF-hand like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.

DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00018; EF HAND; UNKNOWN 3.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON_TER 1
SQ SEQUENCE 518 AA; 58817 MW; 344046C5D6E847B8 CRC64;

Query Match 83.6%; Score 1186; DB 2; Length 518;
Best Local Similarity 81.9%; Pred. No. 3.9e-73;
Matches 222; Conservative 18; Mismatches 31; Indels 0; Gaps 0;

QY 4 QTOISDKYILGRELGRGEGITYLCTDRETRALACKSISKRLRTAVDVEDVRREV 63
DB 33 KARILDKYVLGRELGRGEGITYLCTDRETRALACKSISKRLRTAVDVEDVRREV 92

QY 64 STLPEHPNVVVKATYEDNETVHLMELCEGELFGRIVARGHYTERAAATVARTIAEV 123
DB 93 KHLPEHPNVVVKAGAYEDDNVHLMELCEGELFDRIVARGHYTERGAAQVTRTIVEV 152

QY 124 RMCHVNGVMHRLDKPENFLFANKKENSALKKIDFGLSVLPKGERFTEIVGSPYYMAPEV 183
DB 153 QACHRGVNGVMHRLDKPENFLFANKKENSPLKKAIDFGLSVFPKGERFTEIVGSPYYMAPEV 212

QY 184 LKRNYPGVVDVMSAGVILYLLCGVPPFWAETEQGVVALAILRGVLDKRDPMQISESAK 243
DB 213 LKRNYPGVVDVMSAGVILYLLCGVPPFWAETEQGVVALAILRGVLDKRDPMQISESAK 272

QY 244 SLVKOMLEPDSSTKRLTAQOVLDPHPIQNAK 274
DB 273 SLVRHMLEPDPKARYIAQOVLDPHPIQNAK 303

RESULT 7
Q6NLQ6 PRELIMINARY; PRT; 538 AA.
AC Q6NLQ6; (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE AC3957530.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsia.
OX NCBI_TaxID=3702;
RN [1] SEQUENCE FROM N.A.
RP Cheuk R., Chen H., Kim C.J., Shinn P., Ecker J.R.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN [2] SEQUENCE FROM N.A.
RA Kim C.J., Chen H., Cheuk R., Shinn P., Ecker J.R.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BT012274; AAS76761.1; -.
DR EMBL; BT011630; AAS47636.1; -.
DR HSSP; Q63450; 1A06.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.

DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00018; EF HAND; UNKNOWN 3.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 538 AA; 60935 MW; FADOC733CB85C810 CRC64;

Query Match 81.8%; Score 1161; DB 2; Length 538;
Best Local Similarity 79.5%; Pred. No. 2.1e-71;
Matches 213; Conservative 24; Mismatches 31; Indels 0; Gaps 0;

QY 6 QISDKYILGRLGGEFGITYLCTDRETRALACKSISKRLRTAVDVEDVRREVIMST 65
DB 58 EIESKYTLGRLGGEFGVTVLCTDKETDDVFACKSILKKLRTAVDIEDVRREVEIMRH 117
QY 66 LPEHPNVVVKATYEDNETVHLVLMELCEGGEFGRIIVARGHYTERAAATVARTIAEVVRM 125
DB 118 MPEHPNVVTLKETYEDEHVAHLVLMELCEGGEFGRIIVARGHYTERAAATVKTIMEVQV 177
QY 126 CHVNGVWHRDLKPNFLFANKKENSALKKIDFGLSVLPKGERTEIVGSPYNAPEVLK 185
DB 178 CHKGVWHRDLKPNFLFANKKENSALKKIDFGLSVLPKGERTEIVGSPYNAPEVLK 237
QY 186 RNYGPEVDVMSAGVILVILCGVPPFWAETEQGVALAILRGVLDPKRDPKSOISEAKSL 245
DB 238 RNYGPEVDVMSAGVILVILCGVPPFWAETEQGVALAILRGVLDPKRDPKSOISEAKSL 297

RESULT 8
Q9SCMO PRELIMINARY; PRT; 560 AA.
AC Q9SCMO;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Calcium-dependent protein kinase.
GN Names=T8H10.130;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Benes V., Rechmann S., Borkova D., Ansoorge W., Mewes H.W., Lemcke K.,
RA Mayer K.F.X., Quetier F., Salanoubat M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AL133248; CAB86110.1; -;
DR FIK; T46189; T46189.
DR HSP; P49137; INXK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0006468; P:transferase activity; IEA.
DR InterPro; IPR002048; EF-hand.

DR InterPro; IPR010983; EF Hand like.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00018; EF HAND; UNKNOWN 3.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 560 AA; 63409 MW; 4691E7A7D14B1CD0 CRC64;

Query Match 81.8%; Score 1161; DB 2; Length 560;
Best Local Similarity 79.5%; Pred. No. 2.2e-71;
Matches 213; Conservative 24; Mismatches 31; Indels 0; Gaps 0;

QY 6 QISDKYILGRLGGEFGITYLCTDRETRALACKSISKRLRTAVDVEDVRREVIMST 65
DB 58 EIESKYTLGRLGGEFGVTVLCTDKETDDVFACKSILKKLRTAVDIEDVRREVEIMRH 117
QY 66 LPEHPNVVVKATYEDNETVHLVLMELCEGGEFGRIIVARGHYTERAAATVARTIAEVVRM 125
DB 118 MPEHPNVVTLKETYEDEHVAHLVLMELCEGGEFGRIIVARGHYTERAAATVKTIMEVQV 177
QY 126 CHVNGVWHRDLKPNFLFANKKENSALKKIDFGLSVLPKGERTEIVGSPYNAPEVLK 185
DB 178 CHKGVWHRDLKPNFLFANKKENSALKKIDFGLSVLPKGERTEIVGSPYNAPEVLK 237
QY 186 RNYGPEVDVMSAGVILVILCGVPPFWAETEQGVALAILRGVLDPKRDPKSOISEAKSL 245
DB 238 RNYGPEVDVMSAGVILVILCGVPPFWAETEQGVALAILRGVLDPKRDPKSOISEAKSL 297

RESULT 9
Q48565 PRELIMINARY; PRT; 529 AA.
AC Q48565;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Calcium-dependent protein kinase.
GN Names=MAX17;
OS Fragaria ananassa (Strawberry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid I; Rosales; Rosaceae; Rosoideae; Fragaria.
OX NCBI_TaxID=3747;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fruit;
RA Llop-Tous I., Dominguez-Puigjaner E., Vendrell M.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AF035944; AAB88537.1; -;
DR HSP; P49137; INXK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0006468; P:transferase activity; IEA.
DR InterPro; IPR010983; EF Hand like.
DR InterPro; IPR011009; Kinase like.

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DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD0000012; EF-hand; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN 3.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN 1.
DR PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 529 AA; 59602 MW; 4D3480F527EC5950 CRC64;

Query Match      81.6%; Score 1158; DB 2; Length 529;
Best Local Similarity 79.6%; Pred.No. 3.3e-71;
Matches 215; Conservative 25; Mismatches 30; Indels 0; Gaps 0;

QY 5 TQISDYILGRELGRGFGITLYCTDRETREALACKSISKRLRTAVDVEDVRREVTIMS 64
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
46 TEIEQTYLGRGELGRGFGITLYCTDKATNENYACKSISKQLRTAVDIEDVRREVEIMK 105
QY 65 TLPEHPNVKLYKATYEDNETVHLVLMELCEGGLFGRIVARGHYTERAAATVARTIAEVR 124
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
106 HLPKHPNIYSLKDTYEDDNAVHLVLMELCEGGLFGRIVARGHYTERAAATVARTIAEVR 165
QY 125 MCHVNGVHRDLKPENFLFANKKENSALKAIIDFGLSVLPKPGERFTEIVGSPYYMAPEVL 184
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
166 MCHGVHRDLKPENFLFANKKETAAPLKAIDFGLSVFPKPGERFTEIVGSPYYMAPEVL 225
QY 185 KRYGPEVDVWSAGVILYLLCGVPPFWAETEGQVALAIRGLVDFKRPDPWQSISAKS 244
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
226 RRYGPEVDVWSAGVILYLLCGVPPFWAETEGQVAQAIIRSVDFKRPDPWPKVSDNAKD 285
QY 245 LVKQMLEPDPSTKRLTAQOVLDPHPWIONAKK 274
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
286 LVKQMLDPDPKRLTAQOVLDPHPWIONAKK 315

RESULT 10
Q84SL0 PRELIMINARY; PRT; 550 AA.
ID Q84SL0;
AC Q84SL0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative calcium-dependent protein kinase.
GN Name=OJ1092_A07.132;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]_TaxID=39947;
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC
clone:QJ1092_A07."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AF003966; BAC8205.1; -.
DR HSSP; P49137; INXX.
DR Gramene; Q84SL0; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.

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DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD0000012; EF-hand; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN 4.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN 1.
DR PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 550 AA; 62408 MW; E8AFF800200E0B55 CRC64;

Query Match      81.4%; Score 1155; DB 2; Length 550;
Best Local Similarity 80.6%; Pred.No. 5.5e-71;
Matches 216; Conservative 22; Mismatches 30; Indels 0; Gaps 0;

QY 7 ISDKYILGRELGRGFGITLYCTDRETREALACKSISKRLRTAVDVEDVRREVTIMS 66
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
71 IAARYELGELGRGFGITLYCTERETGDAVACKSISKKLRTAVDIEDVRREVDIMRHL 130
QY 67 PEHPNVKLYKATYEDNETVHLVLMELCEGGLFGRIVARGHYTERAAATVARTIAEVR 126
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
131 PKHPNIVLRTDYEDDNAVHLVLMELCEGGLFGRIVARGHYTERAAATVARTIAEVR 190
QY 127 HVGVMHRDLKPENFLFANKKENSALKAIIDFGLSVLPKPGERFTEIVGSPYYMAPEVL 186
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
191 HKHGVHRDLKPENFLFANKKETAAPLKAIDFGLSVFPKPGERFTEIVGSPYYMAPEVL 250
QY 187 NYGPEVDVWSAGVILYLLCGVPPFWAETEGQVALAIRGLVDFKRPDPWQSISAKSLV 246
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
251 NYGPEVDVWSAGVILYLLCGVPPFWAETEGQVAQAIIRSVDFKRPDPWPRVSDNAKDLV 310
QY 247 KQMLEPDPSTKRLTAQOVLDPHPWIONAKK 274
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
311 KQMLNPDPKRLTAQOVLDPHPWIONAKK 338

RESULT 11
Q8KC54 PRELIMINARY; PRT; 528 AA.
ID Q8KC54;
AC Q8KC54;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Calcium-dependent protein kinase 8.
GN Name=cpk8;
OS Nicotiana plumbaginifolia (leadwort-leaved tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4092;
RN [1]_TaxID=4092;
RP SEQUENCE FROM N.A.
RA Tashiki M.K., Parton R.M., Trewavas A.J.;
RT Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AJ699160; CAG27839.1; -.
DR HSSP; Q63450; 1A06.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:transferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR InterPro; IPR011009; Kinase_like.

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DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR002290; Ser Thr kinase.
 DR InterPro; IPR008271; Ser_thr_kin_AS.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00036; ehand; 4.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000012; EF-hand; 2.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00054; EFh; 4.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; TyrKc; 1.
 DR PROSITE; PS00018; EF HAND; UNKNOWN 3.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN 1.
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase, Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 528 AA; 59419 MW; B10A21C072790CB5 CRC64;

Query Match 80.5%; Score 1142; DB 2; Length 528;
 Best Local Similarity 78.0%; Pred. No. 4.1e-70;
 Matches 209; Conservative 30; Mismatches 29; Indels 0; Gaps 0;

Qy 7 ISDKYILGRLGRGFGITYLCTDRETREALACKSISKRKLTAVDVEDVREVTIMSTL 66
 Db 49 IHDKYDLGRLGRGFGITYLCTDRETREALACKSISKRKLTAVDVEDVREVTIMSTL 108
 Qy 67 PEHNVVVKLKYATYEDNETVHLMELCEGELFGRIVARGHYTERAAATVARTIAEVV 126
 Db 109 PKHPNIVTLKDYEDDNAVHLMELCEGELFGRIVARGHYTERAAATVARTIAEVV 168
 Qy 127 HVNCGVHRDLKPENFLFANKKENSALKAKIDFGLSVLPKPGERFTEIVGSPYMAPEVLKR 186
 Db 169 HRHGVHRDLKPENFLFANKKENSALKAKIDFGLSVLPKPGERFTEIVGSPYMAPEVLKR 228
 Qy 187 NYGEVDVWSAGVILYLLCGVPPFWAETEGVVALAILRGVLDKRPDWPWSOISSAKSLV 246
 Db 229 NYGEVDVWSAGVILYLLCGVPPFWAETEGVVALAILRGVLDKRPDWPWSOISSAKSLV 288
 Qy 247 KQMLEPDSKRLTAQVLDHPWIONAKK 274
 Db 289 KQMLEPDSKRLTAQVLDHPWIONAKK 316

RESULT 12

Q8H1T8 PRELIMINARY; PRT; 522 AA.
 AC Q8H1T8
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 25, Last annotation update)
 DE Calmodulin domain protein kinase 1.
 GN NamesCPK1;
 OS Ceratopteris richardii (Triangle waterfern).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Moniliformopses; Filicophyta; Filicopsida; Filicales; Pteridaceae;
 OC Ceratopteris.
 OX NCBI_TaxID=49495;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gormley M.P., Stout S.C., Roux S.J.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinases family.
 DR EMBL; AY138479; AAN11310.1; --
 DR HSSP; P49137; INXK.
 DR GO; GO:0005224; F:ATP binding; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR010983; EF_Hand_Like.
 DR InterPro; IPR011009; Kinase_Like.
 DR InterPro; IPR000719; Prot_kinase.

DR InterPro; IPR001125; Recoverin.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR008271; Ser_thr_kin_AS.
 DR Pfam; PF00036; ehand; 4.
 DR Pfam; PF00069; Pkinase; 1.
 DR PRINTS; PR00450; RECOVERIN.
 DR ProDom; PD000012; EF-hand; 2.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00054; EFh; 4.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00018; EF HAND; UNKNOWN 3.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN 1.
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase, Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 522 AA; 58780 MW; D94E659C3C1A5CEA CRC64;

Query Match 80.4%; Score 1141; DB 2; Length 522;
 Best Local Similarity 78.6%; Pred. No. 4.8e-70;
 Matches 213; Conservative 25; Mismatches 33; Indels 0; Gaps 0;

Qy 4 QTOISDKYILGRLGRGFGITYLCTDRETREALACKSISKRKLTAVDVEDVREVTIM 63
 Db 44 EQSVNRYHILGRLGRGFGITYLCTDRETREALACKSISKRKLTAVDVEDVREVTIM 103
 Qy 64 STLPEHNVVVKLKYATYEDNETVHLMELCEGELFGRIVARGHYTERAAATVARTIAEVV 123
 Db 104 RHLPPKHPNIVTLGVEYEDENAVHLMELCEGELFGRIVARGHYTERAAATVARTIAEVV 163
 Qy 124 RMCHVNGVHRDLKPENFLFANKKENSALKAKIDFGLSVLPKPGERFTEIVGSPYMAPEV 183
 Db 164 QVCHRGVHRDLKPENFLFANKKENSALKAKIDFGLSVLPKPGERFTEIVGSPYMAPEV 223
 Qy 184 LKRNYPGEVDVWSAGVILYLLCGVPPFWAETEGVVALAILRGVLDKRPDWPWSOISSAK 243
 Db 224 LKRSYSGEVDVWSAGVILYLLCGVPPFWAETEGVVALAILRGVLDKRPDWPWSOISSAK 283
 Qy 244 SLVKQMLEPDSKRLTAQVLDHPWIONAKK 274
 Db 284 ALVRQMLEPDSKRLTAQVLDHPWIONAKK 314

RESULT 13
 Q38873 PRELIMINARY; PRT; 535 AA.
 AC Q38873
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Calmodulin-domain protein kinase CDPK isoform 7 (AT5g19450/F7K24_200)
 DE (Calcium-dependent protein kinase-like protein).
 GN NamesCPK7; Synonyms=At5g12480;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hrabak E.M., Dickmann L.J., Satterlee J.S., Susman M.R.;
 RL MEDLINE=96343943; PubMed=8756605;
 RA "Characterization of eight new members of the calmodulin-like domain protein kinase gene family from Arabidopsis thaliana.";
 RL Plant Mol. Biol. 31:405-412(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Shinn P., Chen H., Cheuk R., Kim C.J., Banh J., Bowser L.,
 RA Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y., Iehida J.,
 RA Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M.,
 RA Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
 RA Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M., Seki M.,
 RA Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K., Davis R.W.,

Qy	187	NYGEVDWSAGVLYL	LLCGVPFFWAE	TEGCV	ALATILRGV	LDFKRPDSQ	ISESAKS	LV	246
Db	230	NYGPEIDWSAGVLYL	LLCGVPFFWAE	TEGCV	ALATILRGV	LDFKRPDPN	ISETAKN	LV	289
Qy	247	KQMLEPDS	TRKLTAAQV	LDPHWI	QNAKK				274
Db	290	RQMLEPDP	KRLRTAKQV	LHPWI	QNAKK				317

Search completed: October 14, 2005, 11:08:43
Job time : 180 secs

RESULT 15	Q8W417	PRELIMINARY;	PRT;	528 AA.
ID	Q8W417			
AC	Q8W417			
DC	01-MAR-2002	(TrEMBLrel. 20, Created)		
DT	01-MAR-2002	(TrEMBLrel. 20, Last sequence update)		
DT	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)		
DE	Calcium-dependent protein kinase.			
GN	Name=At3g51850;			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;			
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsi.			
OX	NCBI_TaxID=3702;			
FN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,			
RA	Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,			
RA	Chen K., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,			
RA	Kim C., Lin X., Liu S.X., Narusaka M., Pham P.K., Sakano H.,			
RA	Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,			
RA	Ecker J., Theologis A., Davis R.W.			
RL	Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,			
RA	Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,			
RA	Deng J.M., Hayashizaki Y., Hsuan V.W., Lee J.M., Ishida J., Kamiya A.,			
RA	Kawai J., Kim C.J., Narusaka M., Onodera C.S., Quach H.L., Sakurai T.,			
RA	Satou M., Seki M., Shinn P., Tang C.C., Torumi M., Wong C., Wu H.C.,			
RA	Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J., Theologis A.,			
RA	Davis R.W.			
RL	Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.			
CC	-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.			
DR	EMBL; AY062533; AAL32617.1; -			
DR	EMBL; BT003367; AAO39985.1; -			
DR	HSSP; P49137; INX.			
DR	GO; GO:0005524; F:ATP binding; IEA.			
DR	GO; GO:0005509; F:calcium ion binding; IEA.			
DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.			
DR	GO; GO:0016740; F:transferase activity; IEA.			
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.			
DR	Pfam; PF00036; ehand; 4.			
DR	Pfam; PF00069; Pkinase; 1.			
DR	ProDom; PD000012; EF-hand; 2.			
DR	ProDom; PD000001; Prot kinase; 1.			
DR	SMART; SM00054; EFh; 4.			
DR	SMART; SM00220; S-TKC; 1.			
DR	PROSITE; PS00018; EF_HAND; UNKNOWN 2.			
DR	PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN 1.			
DR	PROSITE; PS00011; PROTEIN KINASE DOM; 1.			
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.			
KW	ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.			
SEQ	SEQUENCE 528 AA; 59374 MW; E0F0BAFC611626A CRC64;			
Query Match	80.0%;	Score 1135;	DB 2;	Length 528;
Best Local Similarity	78.0%;	Pred. No. 1.2e-69;		
Matches 209;	Conservative 31;	Mismatches 28;	Indels 0;	Gaps 0;
QY	7	ISDKVILGRLGRGFGITLYCTDRETREALACKSISKRKLTAVDVEDVREVTIMSTL	66	
DB	50	IEDRYLLDREILGRGFGVTYLCIERSSRDLLACKSISKRKLTAVDIEDVREVAIMKL	109	
QY	67	PEHPNVVKLKYATYEDNETVHLVWELCEGELFGFRIVARGHYTERAAATVARTIAEVRWC	126	
DB	110	PKSSSIVTLKEACEDDDNAVHLMELCEGELFDRIVARGHYTERAAAGVTKTIVVQLC	169	
QY	127	HVNGVMRDLPENPLFANKKENSALKAIIDFGLSVLFKPGERTFTIVGSPYMAPEVLKR	186	
DB	170	HKHGVIHRLDPENPLFANKKENSPLKAIIDFGLSIFFPKPGKFSFTIVGSPYMAPEVLKR	229	

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OM protein - protein search, using sw model

Run on: October 14, 2005, 10:54:26 ; Search time 166 Seconds
(without alignment)
638.388 Million cell updates/sec

Title: US-08-989-881-2
Perfect score: 1419
Sequence: 1 MANQTQISDKYLGLRELGRG.....TKRLTAQQLVDHPWQNAKK 274

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1419	100.0	274	2	AAW49837 Amino aci
2	1419	100.0	274	4	AAG65757 ATCDPK1a
3	1419	100.0	274	4	AAG65759 ATCDPK1a
4	1318	92.9	274	4	AAG65756 ATCDPK1 k
5	1161	81.8	538	3	AAG43621 Arabidops
6	1161	81.8	538	8	Adh72463 Thale cre
7	1146	80.8	263	7	ABb80250 Fragaria
8	947	66.7	549	5	AAM52842 Physcomit
9	931	65.6	424	3	AAG43622 Arabidops
10	929	65.5	421	3	AAG43623 Arabidops
11	929	65.5	463	3	AAG46565 Arabidops
12	926	65.3	639	5	ABP53637 Maize cal
13	916	64.6	413	4	AAG65755 ATCDPK ki
14	903	63.6	856	3	AAG38599 Arabidops
15	903	63.6	893	3	AAG38598 Arabidops
16	903	63.6	1017	3	AAG38597 Arabidops
17	887.5	62.5	490	8	ADM72386 A. thalia
18	887	62.5	280	4	AAG65758 ATCDPK2 k
19	887	62.5	459	3	AAG29591 Arabidops
20	887	62.5	495	5	AAM48000 Arabidops
21	887	62.5	529	3	AAG29590 Arabidops
22	887	62.5	542	3	AAG29589 Arabidops
23	884	62.3	549	8	AD145327 Rice isop
24	874	61.6	483	3	AAG31158 Arabidops
25	874	61.6	556	3	AAG31157 Arabidops

26	871	61.4	465	8	ADM72385 Maize CDP
27	865	61.0	501	3	AAG35776 Arabidops
28	865	61.0	501	5	AAM48001 Arabidops
29	861.5	60.7	512	2	AAW93256 Soybean C
30	819	57.7	569	2	AAW56237 Protein k
31	757	53.3	404	3	AAG46566 Arabidops
32	710	50.0	408	3	AAG31159 Arabidops
33	710	50.0	597	5	AAM52841 Physcomit
34	706	49.8	425	3	AAG35777 Arabidops
35	706	49.8	523	8	ADN73153 Thale cre
36	699	49.3	523	3	AAG10101 Arabidops
37	697	49.1	623	4	AAW85583 Rice CDPK
38	697	49.1	623	5	ABP53630 Arabidops
39	690	48.6	625	5	ABP53638 Maize cal
40	689	48.6	483	7	ADC07764 Rice prot
41	688	48.5	599	7	ADL06615 Tobaccoc
42	685	48.3	378	3	AAG46567 Arabidops
43	682	48.1	386	8	ADM72366 Soybean C
44	676	47.6	576	5	ABP53639 A. thalia
45	648.5	45.7	416	8	ADM72364 Soybean C

ALIGNMENTS

RESULT 1

AAW49837
ID AAW49837 standard; protein; 274 AA.

XX AAW49837;

XX 27-AUG-2003 (revised)

DT 12-OCT-1998 (first entry)

XX Amino acid sequence of ATCDPK1a PK domain.

DE ATCDPK1a; protein kinase; PK; tolerance; drought; salinity; cold; heat;

KW fruit; ornamental; vegetable; cereal; field crops.

XX Arabidopsis sp.

XX WO9826045-A1.

XX 18-JUN-1998.

PF 12-DEC-1997; 97WO-US023019.

XX 13-DEC-1996; 96US-0032966P.

PR (GEHO) GEN HOSPITAL CORP.

XX Sheen J;

DR WPI; 1998-348509/30.

XX N-PSDB; AAV36878.

PT Protecting plants against environmental stress - by introducing protein kinase domain-containing gene, calcium dependent protein kinase gene or calcium/calmodulin-dependent gene.

XX Claim 22; Fig 5; 62pp; English.

CC This is the amino acid sequence of the ATCDPK1a protein kinase (PK) domain isolated from the Arabidopsis cDNA library, and used in the method of the invention to protect plants against environmental stress. The methods can be used for improving the tolerance of plants to environmental stresses such as drought, salinity, cold and heat. They provide for increased production efficiency, as well as for improvements in quality and the yield of crop plants and ornamentals. The methods contribute to the production of high quality and high yield agricultural products, e.g. fruits, ornamentals, vegetables, cereals, and field crops.

CC (Updated on 27-AUG-2003 to correct OS field.)

CC library member is expressed in the plant protoplasts); and (2) screening
 CC the protoplasts to determine whether the amount of gene expression of the
 CC reporter gene construct changes in response to the expression of the
 CC library members, a change in gene expression of the reporter gene
 CC construct identifying the gene product expressed by the library member as
 CC 1 that modulates expression of the gene of interest. The present sequence
 CC represents the amino acid sequence of Arabidopsis calcium dependant
 CC protein kinase (CDPK) ATCDPK1a PK domain
 XX Sequence 274 AA;

Query Match 100.0%; Score 1419; DB 4; Length 274;
 Best Local Similarity 100.0%; Pred. No. 5.4e-146;
 Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANOTQISDKYILGRELGRGFGITVLTCTDRETRALACKSISKRLRTAVDVEDVRREV 60
 DB 1 MANOTQISDKYILGRELGRGFGITVLTCTDRETRALACKSISKRLRTAVDVEDVRREV 60

QY 61 TIMSTLPEHPNVVVKLKYEDNETVHLMELCEGELFGRIIVARGHYTERAAATVARTIA 120
 DB 61 TIMSTLPEHPNVVVKLKYEDNETVHLMELCEGELFGRIIVARGHYTERAAATVARTIA 120

QY 121 EYVRMCHVNGVMHRDLKPENFLFANKKENSALKKIDFGLSVLPKGERFTEIVGSPYYMA 180
 DB 121 EYVRMCHVNGVMHRDLKPENFLFANKKENSALKKIDFGLSVLPKGERFTEIVGSPYYMA 180

QY 181 PEVLKRNYPGVVDVMSAGVILYLLCGVPPFWAETEQGVVALAILRGVLDPKRDPWSQISE 240
 DB 181 PEVLKRNYPGVVDVMSAGVILYLLCGVPPFWAETEQGVVALAILRGVLDPKRDPWSQISE 240

QY 241 SAKSLVKOMLEPDPSTKRLTAQQVLDHPWIONAKK 274
 DB 241 SAKSLVKOMLEPDPSTKRLTAQQVLDHPWIONAKK 274

RESULT 4
 AAG65756
 ID AAG65756 standard; protein; 274 AA.
 XX
 AC AAG65756;
 DT 07-JAN-2002 (first entry)
 XX
 DE ATCDPK1 kinase domain sequence.
 XX
 KW Plant protoplast; gene expression; Arabidopsis; PK; CDPK; ATCDPK1;
 KW calcium activated protein kinase; calcium dependant protein kinase.
 OS Arabidopsis thaliana.
 XX
 PN WO200168920-A1.
 XX
 PD 20-SEP-2001.
 XX
 PF 13-MAR-2001; 2001WO-US007999.
 XX
 PR 13-MAR-2000; 2000US-0189074P.
 XX
 PA (GENO) GEN HOSPITAL CORP.
 PI Sheen J;
 XX
 DR WPI; 2001-611395/70.
 XX
 PT Using plant protoplast expression systems for rapidly screening libraries
 PT of nucleic acids to identify gene that modulate expression of target
 PT genes.
 XX
 PS Example; Fig 3B; 95pp; English.
 XX
 CC The invention provides a high through-put assay for rapidly screening a
 CC library of nucleic acid molecules to identify a gene product that

CC modulates expression of a gene of interest in plant protoplasts. The
 CC method comprises: (1) introducing into 1 or more plant protoplasts: (a) a
 CC reporter gene construct operably linked to a promoter of a gene of
 CC interest; and (b) a member of a library of nucleic acid molecules (the
 CC library member is expressed in the plant protoplasts); and (2) screening
 CC the protoplasts to determine whether the amount of gene expression of the
 CC reporter gene construct changes in response to the expression of the
 CC library members, a change in gene expression of the reporter gene
 CC construct identifying the gene product expressed by the library member as
 CC 1 that modulates expression of the gene of interest. The present sequence
 CC represents the amino acid sequence of Arabidopsis calcium dependant
 XX protein kinase (CDPK) ATCDPK1 kinase domain
 XX Sequence 274 AA;

Query Match 92.9%; Score 1318; DB 4; Length 274;
 Best Local Similarity 92.0%; Pred. No. 5.8e-135;
 Matches 252; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 1 MANOTQISDKYILGRELGRGFGITVLTCTDRETRALACKSISKRLRTAVDVEDVRREV 60
 DB 1 MSNQTQISDKYILGRELGRGFGITVLTCTDRETRALACKSISKRLRTAVDVEDVRREV 60

QY 61 TIMSTLPEHPNVVVKLKYEDNETVHLMELCEGELFGRIIVARGHYTERAAATVARTIA 120
 DB 61 AIMSTLPEHPNVVVKLKYEDNETVHLMELCEGELFGRIIVARGHYTERAAATVARTIA 120

QY 121 EYVRMCHVNGVMHRDLKPENFLFANKKENSALKKIDFGLSVLPKGERFTEIVGSPYYMA 180
 DB 121 EYVRMCHVNGVMHRDLKPENFLFANKKENSALKKIDFGLSVLPKGERFTEIVGSPYYMA 180

QY 181 PEVLKRNYPGVVDVMSAGVILYLLCGVPPFWAETEQGVVALAILRGVLDPKRDPWSQISE 240
 DB 181 PEVLKRNYPGVVDVMSAGVILYLLCGVPPFWAETEQGVVALAILRGVLDPKRDPWSQISE 240

QY 241 SAKSLVKOMLEPDPSTKRLTAQQVLDHPWIONAKK 274
 DB 241 SAKSLVKOMLEPDPSTKRLTAQQVLDHPWIONAKK 274

RESULT 5
 AAG43621
 ID AAG43621 standard; protein; 538 AA.
 XX
 AC AAG43621;
 XX
 DT 18-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 54544.
 XX
 KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX
 OS Arabidopsis thaliana.
 XX
 PN EP1033405-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 25-FEB-2000; 2000EP-00301439.
 XX
 PR 25-FEB-1999; 99US-0121825P.
 PR 05-MAR-1999; 99US-0123180P.
 PR 09-MAR-1999; 99US-0123548P.
 PR 23-MAR-1999; 99US-0125788P.
 PR 25-MAR-1999; 99US-0126264P.
 PR 29-MAR-1999; 99US-0126785P.
 PR 01-APR-1999; 99US-0127482P.
 PR 06-APR-1999; 99US-0128234P.
 PR 08-APR-1999; 99US-0128714P.
 PR 16-APR-1999; 99US-0129845P.
 PR 19-APR-1999; 99US-0130077P.

PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-01311449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-01343768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
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PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
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PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
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PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140961P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142300P.
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PR 09-JUL-1999; 99US-0142920P.
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PR 16-JUL-1999; 99US-0144086P.
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PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
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PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
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PR 03-AUG-1999; 99US-0147038P.
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PR 04-AUG-1999; 99US-0147302P.
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PR 06-AUG-1999; 99US-0147303P.
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PR 09-AUG-1999; 99US-0147935P.
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PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
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PR 18-AUG-1999; 99US-0149426P.
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PR 20-SEP-1999; 99US-0154779P.
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PR 23-SEP-1999; 99US-0155486P.
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PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
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PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158212P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.

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PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match      81.8%; Score 1161; DB 3; Length 538;
Best Local Similarity 79.5%; Pred. No. 2.3e-117;
Matches 213; Conservative 24; Mismatches 31; Indels 0; Gaps 0;

QY 6 QISDKYILGRLGRGFGITYLCTDRETREALACKSISKRKLRTAVDVEDVRREVTIMST 65
DB 58 EIESKYTLGRLGRGFGVYLYLCTDKETDDVFACKSILKKLRTAVDIEDVREVEIMRH 117
QY 66 LPEHNVVKLKATYEDNETVHLMELCEGGEFGRIIVARGHYTERAAATVARTIAEVVRM 125
DB 118 MPEHNVVTLKETYEDEHAHVLVLMELCEGGEFGFDRIVARGHYTERAAAAVTKTIMEVQV 177
QY 126 CHVNGVMHRDLKPNFLFANKKENSALKAIIDFGLSVLPKPGERFTEIVGSPYMAPEVLK 185
DB 178 CHKGVMHRDLKPNFLFNGKKTAPLKAIDFGLSVFPKPGERFNEIVGSPYMAPEVLK 237
QY 186 RNYGPEVDVWSAGVILYILLCGVPPFWAETEGQVALAILRGVLDKFRDPWSQISBSAKSL 245
DB 238 RNYGPEVDVWSAGVILYILLCGVPPFWAETEGQVAQAIIRSVLDFRDPWPKVSENAKDL 297
QY 246 VKQMLEPSTKRLTAQQVLDHPWIONAK 273
DB 298 IRKMLDPDQKRRLLTAQQVLDHPWLQNAK 325

RESULT 6
ADN72463
ID ADN72463 standard; protein; 538 AA.
XX
AC ADN72463;
XX
DT 15-JUL-2004 (first entry)
XX
DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 359.
XX
KW plant; transgenic; E2Fa/Dpa transcription factor; growth regulator;
KW animal feed product; thale cress; cell wall biosynthesis;
KW nitrogen metabolism; carbon metabolism.
XX
OS Arabidopsis thaliana.
XX
FN WO2004035798-A2.
XX
PD 29-APR-2004.
XX
PF 20-OCT-2003; 2003WO-EP011658.
XX
PR 18-OCT-2002; 2002EP-00079408.
XX

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PA (CROP-) CROPDESIGN NV.
XX Inze D, De Veylder L, Vlieghe K;
XX WPI; 2004-348466/32.
DR N-PSDB; ADN72462.
XX
PT Altering plant characteristics, useful for producing plants for enzyme or
PT pharmaceutical production comprises modifying in a plant, expression of
PT one or more nucleic acids and/or modifying level or activity of one or
PT more proteins.
XX
PS Claim 1; SEQ ID NO 358; 134pp; English.
XX
CC This invention relates to a novel method for altering one or more plant
CC characteristics. Specifically, it refers to identifying genes that are up
CC - or down-regulated in transgenic plants overexpressing the heterodimeric
CC E2Fa/Dpa transcription factor of Arabidopsis and using these sequences to
CC alter plant characteristics accordingly. The present invention describes
CC generating transgenic plants for the production of growth regulators,
CC enzymes, therapeutics, pharmaceuticals and animal feed products, where
CC the altered plant characteristics are selected from increased yield or
CC biomass, enhanced survival capacity, stress tolerance, plant architecture
CC or physiology, altered endoreduplication, biochemistry, signal
CC transduction, storage lipid mobilisation and/or altered photosynthesis,
CC each relative to the corresponding wild type plants. Accordingly, these
CC sequences can also be useful as positive or negative selectable markers
CC during transformation of cells or tissues. The identified genes play a
CC role in a variety of biological processes such as DNA replication, cell
CC wall biosynthesis, nitrogen and/or carbon metabolism or they function as
CC transcription factors. This polypeptide sequence is thale cress protein
CC expressed by a gene upregulated 1.3 fold or more in plants overexpressing
CC the E2Fa/Dpa transcription factor, given in an exemplification of the
CC invention.
XX
SQ Sequence 538 AA;

Query Match      81.8%; Score 1161; DB 8; Length 538;
Best Local Similarity 79.5%; Pred. No. 2.3e-117;
Matches 213; Conservative 24; Mismatches 31; Indels 0; Gaps 0;

QY 6 QISDKYILGRLGRGFGITYLCTDRETREALACKSISKRKLRTAVDVEDVRREVTIMST 65
DB 58 EIESKYTLGRLGRGFGVYLYLCTDKETDDVFACKSILKKLRTAVDIEDVREVEIMRH 117
QY 66 LPEHNVVKLKATYEDNETVHLMELCEGGEFGRIIVARGHYTERAAATVARTIAEVVRM 125
DB 118 MPEHNVVTLKETYEDEHAHVLVLMELCEGGEFGFDRIVARGHYTERAAAAVTKTIMEVQV 177
QY 126 CHVNGVMHRDLKPNFLFANKKENSALKAIIDFGLSVLPKPGERFTEIVGSPYMAPEVLK 185
DB 178 CHKGVMHRDLKPNFLFNGKKTAPLKAIDFGLSVFPKPGERFNEIVGSPYMAPEVLK 237
QY 186 RNYGPEVDVWSAGVILYILLCGVPPFWAETEGQVALAILRGVLDKFRDPWSQISBSAKSL 245
DB 238 RNYGPEVDVWSAGVILYILLCGVPPFWAETEGQVAQAIIRSVLDFRDPWPKVSENAKDL 297
QY 246 VKQMLEPSTKRLTAQQVLDHPWIONAK 273
DB 298 IRKMLDPDQKRRLLTAQQVLDHPWLQNAK 325

RESULT 7
ABB80250
ID ABB80250 standard; protein; 263 AA.
XX
AC ABB80250;
XX
DT 18-DEC-2003 (first entry)
XX
DE Fragaria CamK.
XX
KW Calcium/calmodulin-dependant protein kinase; CamK; fungicide;

```


KW fungal growth; development; inhibition.
XX Fragaria x ananassa.
XX WO2003076582-A2.
XX 18-SEP-2003.
XX 06-MAR-2003; 2003WO-US006935.
XX 06-MAR-2002; 2002US-0362008P.
XX 21-MAR-2002; 2002US-0366504P.
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX (REGC) UNIV CALIFORNIA.
XX (JUDE/) JUDELSON H S.
XX Judelson HS;
XX WPI; 2003-731821/69.
XX
XX Identifying a fungicidal compound comprises combining a polypeptide with
XX the compound to be tested with the ability to bind, or to inhibit the
XX activity of the polypeptide under conditions conducive to binding or
XX inhibition.
XX
XX Disclosure; Fig 3c; 105pp; English.
XX
XX The sequences given in ABB80245-52 shows calcium/calmodulin-dependant
XX protein kinases (CaMK) from various animals which are included for
XX comparison with the P. infestans CaMK of the invention. The CaMK gene is
XX expressed as an intron-lacking transcript bearing 5' and 3' untranslated
XX regions of 50 and 45 nt, respectively. CaMK plays a role in fungal growth
XX and development. The CaMK protein may be used in the method of the
XX invention for identifying a fungicidal compound. The method comprises
XX combining the CaMK polypeptide with the compound to be tested with the
XX ability to bind, or to inhibit the activity of the polypeptide under
XX conditions conducive to binding or inhibition. The method is useful for
XX identifying compounds that interact with or inhibit the proteins
XX essential for fungal growth, which are thus useful as fungicides. The
XX proteins are useful for in vitro assays for screening fungicidal
XX chemicals whose targets has not been identified to determine if they
XX inhibit protein activity, and for elucidating the complex structures of
XX these molecule and to further characterize their association with known
XX inhibitors in order to rationally design new inhibitory herbicides
XX
XX Sequence 263 AA;
XX
XX Query Match 80.8%; Score 1146; DB 7; Length 263;
XX Best Local Similarity 81.0%; Pred. No. 3.4e-116; Indels 0; Gaps 0;
XX Matches 213; Conservative 23; Mismatches 27;
XX
XX 11 YILGRELGRGFGITYLCTDRETRALACKSISKRKLRTAVDVEDVREVTINSTLPEHP 70
XX 1 YELGRELGRGFGITYLCTDRTATNENYACKSISKQKLTAVDIEDVREVEIMKHLPGHP 60
XX
XX 71 NVVKLKATYENETVHLVMECEGELPGRIVARGHYTERAAATVARTIARVVMCHVNG 130
XX 61 NIVSLKDTYEDDNVHLVMECEGELPDRIVSRGHYTERAAATVKTIVVQMCHKHG 120
XX 131 VMHRLDKPENFLFANKKNSALKKIDFGLSVLPKPGERTFIVGSPYMAPEVLKRYNGP 190
XX 121 VMHRLDKPENFLFANKKETAPLKIDFGLSVFPKPGERTFIVGSPYMAPEVLKRYNGP 180
XX
XX 191 EVDVMSAGVILYILCGVPPFWAETEQQVALAILRGVLDKFRDPSQTSSEAKSLVKQML 250
XX 181 EVDVMSAGVILYILCGVPPFWAETEQQGVAIIRSVVDFKRDWPKVSDNAKDLVKQML 240
XX 251 EPDSTKRLTAQOVLDPHPIQNAK 273
XX 241 DDPKRLTAQOVLDPHTLQNAK 263

RESULT 8
AAM52842
ID AAM52842 standard; protein; 549 AA.
XX
XX AAM52842;
XX
XX 22-FEB-2002 (first entry)
XX
XX Physcomitrella patens CPK-2 protein, SEQ ID NO:39.
XX
XX Protein kinase stress-related protein; PKSRP; moss; protein kinase-6;
XX PK-6; protein kinase-7; PK-7; protein kinase-8; PK-8; protein kinase-9;
XX PK-9; casein kinase homologue-1; CK-1; casein kinase homologue-2; CK-2;
XX casein kinase homologue-3; CK-3; mitogen-activated protein kinase;
XX MAP kinase-2; MPK-2; MAP kinase-3; MPK-3; MAP kinase-4; MPK-4;
XX MAP kinase-5; MPK-5; calcium-dependent protein kinase-1; CPK-1;
XX calcium-dependent protein kinase-2; CPK-2; overexpression;
XX environmental stress; salinity; drought; temperature; tolerance;
XX transgenic plant; EST; expressed sequence tag.
XX
XX Physcomitrella patens.
XX
XX WO200177356-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-US011435.
XX
XX 07-APR-2000; 2000US-0196001P.
XX
XX (BADI) BASF PLANT SCI GMBH.
XX
XX Da Costa E SilvaO, Bohnert HJ, Van Thiel N, Chen R;
XX Sarria-Millan R;
XX WPI; 2002-049153/06.
XX N-PSDB; ABA91081.
XX
XX New protein, useful for increasing tolerance to environmental stress,
XX comprises a Protein Kinase Stress-Related Protein selected from Protein
XX kinases, Casein kinase homologs, MAP kinases or Calcium dependent protein
XX kinases.
XX
XX Claim 13; Fig 3M; 154pp; English.
XX
XX Sequences AAM52830-AAM52842 represent novel protein kinase stress-related
XX proteins (PKSRPs) from the moss Physcomitrella patens, and sequences
XX ABA91069-ABA91081 represent full-length cDNAs encoding them. The cDNA
XX sequences were obtained from expressed sequence tags (ESTs; ABA91056-
XX ABA91068) derived from Physcomitrella patens cDNA libraries. The PKSRPs
XX of the invention comprise protein kinase-6 (PK-6), protein kinase-7 (PK-
XX 7), protein kinase-8 (PK-8), protein kinase-9 (PK-9), casein kinase
XX homologue-1 (CK-1), casein kinase homologue-2 (CK-2), casein kinase
XX homologue-3 (CK-3), mitogen-activated protein (MAP) kinase-2 (MPK-2), MAP
XX kinase-3 (MPK-3), MAP kinase-4 (MPK-4), MAP kinase-5 (MPK-5), calcium-
XX dependent protein kinase-1 (CPK-1), and calcium-dependent protein kinase-
XX 2 (CPK-2). When overexpressed, the PKSRPs are able to confer tolerance to
XX environmental stresses such as salinity, drought, temperature, metal,
XX chemical, pathogenic and oxidative stress. Physcomitrella patens PKSRP
XX nucleic acids may be used to generate transgenic plants and seeds with
XX increased tolerance to salinity, drought and temperature. The transgenic
XX plants generated can be monocots or dicots and are especially maize,
XX wheat, rye, oat, triticale, rice, barley, cotton, rapeseed, cassava,
XX sunflower, tagetes, leguminous plants (e.g., soybean, peanut, vicia
XX species, alfalfa), solanaceous plants (e.g., potato, tobacco, aubergine,
XX pepper, tomato), coffee, cacao, tea, Salix species, oil palm, coconut,
XX perennial grasses and forage crops. The PKSRP nucleotide and proteins may
XX also be used in evolutionary and protein structural studies and as
XX markers for specific regions of the genome
XX
XX Sequence 549 AA;

Query Match 66.7%; Score 947; DB 5; Length 549;

Best Local Similarity 66.2%; Pred. No. 5.7e-94;		Matches 176; Conservative 35; Mismatches 55; Indels 0; Gaps 0;	
Qy	5	TQISDKVILGRELGRGEGITYLCTDRETRREALACKSISKRKURTAVDVEDVREVTIMS 64	
Db	87	SDIROSYILGRELGRGQFGVYLTCDKMTNEAYACKSIKRLTSKEDIEDVKREYQIMH 146	
Qy	65	TLPEHNPVKLKATYEDNETVHLVLMELCEGGLFGRIVARGHYTERAAATVARTIAEVVR 124	
Db	147	HLSGTENIVLVKDVFDKSHVHLVLMELCAGGELFDRIIAKGYHSERAAADMCRVIVNVH 206	
Qy	125	MCHVNGMHRDLKPNFLFANKKENSALKAKAIDFGLSVLPKPGERFTEIVGSPYYMAPEVL 194	
Db	207	RCHSLGVFHRDLKPNFLFANKKENSALKAKAIDFGLSVLPKPGERFTEIVGSPYYMAPEVL 266	
Qy	185	KRNYGPEVDVWSAGVILYLLCGVPPFWAETEGQVALAILRGVLDPKRDPWSOISSAKS 244	
Db	267	KRSYGPEADVWSAGVIVYLLCGVPPFWAETEGQIFDAVLKGHIDFENDFPKPKISGAKD 326	
Qy	245	LVKOMLEPDPSTKRLTAQOVLDPHPIQ 270	
Db	327	LVKMLNPVNKRLTAQOVLDPHPIQ 352	
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ID	AAG43622 standard; protein; 424 AA.		
AC	AAG43622;		
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DT	18-OCT-2000 (first entry)		
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DE	Arabidopsis thaliana protein fragment SEQ ID NO: 54545.		
XX			
KW	Protein identification; signal transduction pathway; metabolic pathway;		
KW	hybridisation assay; genetic mapping; gene expression control; promoter;		
KW	termination sequence.		
XX			
OS	Arabidopsis thaliana.		
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PN	EP1033405-A2.		
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PD	06-SEP-2000.		
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PF	25-FEB-2000; 2000EP-00301439.		
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Best Local Similarity 80.6%; Pred. No. 2.2e-92;		
Matches 170; Conservative 18; Mismatches 23; Indels 0; Gaps 0;		
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Qy	123	VRMCHVNGVMHRDLKPFENFLFANKKENSALKAIIDFGLSVLFKPGERFTEIVGSPYYMAPE 182
Db	61	VQVCHKGVMHRDLKPFENFLFGNKKETAPLKAIDFGLSVFVKPGERFNEIVGSPYYMAPE 120
Qy	183	VLKRNYPGEVDVWSAGVILYLILCGVPPFWAETEQGVVALAILRGVLDPKRDPMSQISESA 242
Db	121	VLKRNYPGEVDIWSAGVILYLILCGVPPFWAETEQGVAAIIRSVLDFRRDPWPVKVSENA 180
Qy	243	KSLVKOMLEPDKRLTAQOVLDPHPWIONAK 273
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XX	AC AAG43623;	
XX	DT 18-OCT-2000 (first entry)	
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 54546.	
KW	Protein identification; signal transduction pathway; metabolic pathway;	
KW	hybridisation assay; genetic mapping; gene expression control; promoter;	
XX	termination sequence.	
OS	Arabidopsis thaliana.	
PN	EP1033405-A2.	
PD	06-SEP-2000.	
PF	25-FEB-2000; 2000EP-00301439.	
XX	25-FEB-1999; 99US-0121825P.	
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Best Local Similarity 63.6%; Score 903; DB 3; Length 856;

Matches 173; Conservative 29; Mismatches 58; Indels 12; Gaps 1;

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AC AAG38598;
XX
DT 18-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 47641.
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XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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OS Arabidopsis thaliana.
XX
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Query Match 63.6%; Score 903; DB 3; Length 893;

Best Local Similarity 63.6%; Pred. No. 7.6e-89;

Matches 173; Conservative 29; Mismatches 58; Indels 12; Gaps 1;

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Job time : 170 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 10:40:31 ; Search time 21 Seconds
(without alignments)
973.993 Million cell updates/sec

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	871	61.4	464	3	US-08-459-504B-22
7	871	61.4	464	3	US-08-459-444-22
8	871	61.4	464	3	US-09-547-422-22
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ALIGNMENTS

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; Patent No. 6262345
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/347,801
; CURRENT FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: 60/092,438
; EARLIER FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 17
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Zea mays
US-09-347-801-17

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; Patent No. 6794561							

GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Lee, Jian Ming
TITLE OF INVENTION: Plant Protein Kinases
FILE REFERENCE: BB-1171
CURRENT APPLICATION NUMBER: US/09/854,731
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: 60/092,438
PRIOR FILING DATE: July 10, 1998
SOFTWARE: Microsoft Office 97
SEQ ID NO 17
LENGTH: 639
TYPE: PRT
ORGANISM: Zea mays
US-09-854-731-17

Query Match 65.3%; Score 926; DB 4; Length 639;
Best Local Similarity 65.5%; Pred. No. 1.6e-86;
Matches 173; Conservative 31; Mismatches 60; Indels 0; Gaps 0;

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Sequence 22, Application US/07951715A
Patent No. 5625136
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lytle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/951,715A
FILING DATE: 25-SEP-1992
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8615
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..464
OTHER INFORMATION: /note= "derived protein sequence of
OTHER INFORMATION: pollen specific CDPK as disclosed in Figure 34."
US-07-951-715A-22

Query Match 61.4%; Score 871; DB 1; Length 464;
Best Local Similarity 63.1%; Pred. No. 4.8e-81;
Matches 164; Conservative 31; Mismatches 65; Indels 0; Gaps 0;

Qy 11 YILGRLGRGFGITVCTDRETRALACKSISKRKLRTAVDVEDVRREVTIMSTLPEHP 70
Db 13 YSMGKELGRGQFGVTHLCTHRTSGKLACKTIARKLAAEDVDVRRREVOIMHLSGQP 72

Qy 71 NVVKLKATYEDNETVHLMELCGGELFGRIVARHYTERAAATVARTIAEVVRCMVNG 130
Db 73 NVVGLRGAYEDKQSVHLMELCAGGELFDRILARGQYTERGAELRLRAIVQVHTCHSMG 132

Qy 131 VMHRDLKPENFLFANKKENSALKKIDFGLSVLPKPGERFTEIVGSPYMAPEVLKRYGP 190
Db 133 VMHRDLKPENFLFLLSKDEDAPLKATDFGLSVFFKEGELLRDIVGSAYYIAPEVLKRYGP 192

Qy 191 EVDVWSAGVILYLLCGVPPFWAETEGVALAILRGVLDPKRDPWQISSEAKSLVKQML 250
Db 193 EADIVSGVNLVIFLAGVPPFWAENENGIFTAILRGOLDLSSEPPWPHISPGAKDLVKQML 252

Qy 251 EPDSTKRLTAQOVLDPHIQ 270
Db 253 NINPKRLTAQOVLDPHIQ 272

RESULT 4
US-08-459-448A-22
Sequence 22, Application US/08459448A
Patent No. 5859336
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lytle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.

COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,444A
FILING DATE: 02-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805/PI/CGC1577/CIP/DIV6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: /note= "derived protein sequence of
pollen specific CDPK as disclosed in Figure 34."
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..464
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-08-459-444-22

Query Match 61.4%; Score 871; DB 3; Length 464;
Best Local Similarity 63.1%; Pred. No. 4.8e-81;
Matches 164; Conservative 31; Mismatches 65; Indels 0; Gaps 0;
QY 11 YILGRELGRGEGITVLTCTDRETRALACKSISKRLTAVDVEDVRREVTIMSTLPEHP 70
DB 13 YSMGKELGRGQGVTHLCTHRTSGEKLACKTIARKLAAAREDDVDVRREVMHLSGQP 72
QY 71 NVVKLKATYEDNETVHLMELCEGELFGRIVARGHYTERAAATVARTIAEVRMCHVNG 130
DB 73 NVVGLRGAYEDKQSVHLMELCAGGELFDRIIARGQYTERGAELRLAIQIVHTCHSMG 132
QY 131 VMHRDLKPNFLFANKKENSALKAIIDFGLSVLFKPGERFTEIVGSPYYMAPEVLKRNYP 190
DB 133 VMHRDIKPNFLLSKDEADAPLKATDFGLSVFFKEGELLRDIVGSAYYIAEVLKRYGP 192
QY 191 EVDVWSAGVILYLLCGVPPFWAETEOGVVALILRGVLDKFDKDPWSQISESAKSLVKOML 250
DB 193 EADIWSGVMLYIFLAGVPPFWAENENGIFTAILRGQLDLSSEPPPHISPGAKDLVKKML 252
QY 251 EPDSTKRLTAQVLDHPHIQ 270
DB 253 NINPKERLTAFOVLNHPWK 272

RESULT 8

US-09-547-422-22
Sequence 0, Application US/09547422
Patent No. 6320100
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.

Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Lauelis, Karen L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6320100artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,422
FILING DATE: 11-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805H
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: /note= "derived protein sequence of
pollen specific CDPK as disclosed in Figure 34."
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..464
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-547-422-22
Query Match 61.4%; Score 871; DB 3; Length 464;
Best Local Similarity 63.1%; Pred. No. 4.8e-81;
Matches 164; Conservative 31; Mismatches 65; Indels 0; Gaps 0;
QY 11 YILGRELGRGEGITVLTCTDRETRALACKSISKRLTAVDVEDVRREVTIMSTLPEHP 70
DB 13 YSMGKELGRGQGVTHLCTHRTSGEKLACKTIARKLAAAREDDVDVRREVMHLSGQP 72
QY 71 NVVKLKATYEDNETVHLMELCEGELFGRIVARGHYTERAAATVARTIAEVRMCHVNG 130
DB 73 NVVGLRGAYEDKQSVHLMELCAGGELFDRIIARGQYTERGAELRLAIQIVHTCHSMG 132
QY 131 VMHRDLKPNFLFANKKENSALKAIIDFGLSVLFKPGERFTEIVGSPYYMAPEVLKRNYP 190
DB 133 VMHRDIKPNFLLSKDEADAPLKATDFGLSVFFKEGELLRDIVGSAYYIAEVLKRYGP 192
QY 191 EVDVWSAGVILYLLCGVPPFWAETEOGVVALILRGVLDKFDKDPWSQISESAKSLVKOML 250
DB 193 EADIWSGVMLYIFLAGVPPFWAENENGIFTAILRGQLDLSSEPPPHISPGAKDLVKKML 252

Qy 251 EPDSTKRLTAQQVLDHPWQ 270
Db 253 NINPKERLTAFOVLNHPWK 272

RESULT 9

US-09-988-462-22
; Sequence 22, Application US/09988462
; Patent No. 6720488
; GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Lauis, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: Syngenta Biotechnology, Inc.
STREET: 3054 Cornwalis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/988 462

FILING DATE: 20-NOV-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/547,422

FILING DATE: 11-APR-2000

APPLICATION NUMBER: US 08/459,504

FILING DATE: 02-JUN-1995

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: S-188051

TELEPHONE: (919) 541-8587

TELEFAX: (919) 541-8689

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 464 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: Protein

LOCATION: 1..464

OTHER INFORMATION: /note= "derived protein sequence of

pollen specific CDPK as disclosed in Figure 34."

SEQUENCE DESCRIPTION: SEQ ID NO: 22:

US-09-988-462-22

Query Match

Best Local Similarity

61.4%; Score 871; DB 4; Length 464;

63.1%; Pred. No. 4.8e-81;

Matches 164; Conservative 31; Mismatches 65; Indels 0; Gaps 0;
Qy 11 YILGRELGRGFGITYLCTDRETRALACKSISKRLRTAVDVEDVREVTIMSTLPEHP 70
Db 13 YSMGKELGRGQFGVTHLCTHRTSGEKLAACKTKAKRKLAAAREDDVDRREVQIMHLSGQP 72
Qy 71 NVVKLKATYEDNETVHLMELCEGELFGRIVARGHYTERAAATVARTIAEVVRMCHVNG 130
Db 73 NVVGLRGAYEDKQSVHLMELCAGGELFDRITARGQYTERGAELLRRAIVQIVHTCHSMG 132
Qy 131 VMHRDLKPENFLFANKKENSALKADFDGLSVLFKPGERFTEIVGSPYMAPEVLKRYGP 190
Db 133 VMHRDIKPENFLLSKDEADAPLXATDFGLSVFVKGELLARDIVGSAYYIAPEVLKRYGP 192
Qy 191 EVDVMSAGVILYLLCGVPPFWAETGQVALAILRGVLDFKRDPMQISAKSLVKQML 250
Db 193 EADINSVGVMLYIFLAGVPPFWAENENGIFTAILRGQLDLSBEPWPHISPGAKDLVKQML 252
Qy 251 EPDSTKRLTAQQVLDHPWQ 270
Db 253 NINPKERLTAFOVLNHPWK 272

RESULT 10

US-07-951-715A-25

; Sequence 25, Application US/07951715A

; Patent No. 5625136

; GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.

APPLICANT: Desai, Nalini M.

APPLICANT: Lewis, Kelly S.

APPLICANT: Kramer, Vance C.

APPLICANT: Warren, Gregory W.

APPLICANT: Evola, Stephen V.

APPLICANT: Crossland, Lyle D.

APPLICANT: Wright, Martha S.

APPLICANT: Merlin, Ellis J.

APPLICANT: Lauis, Karen L.

APPLICANT: Rothstein, Steven J.

APPLICANT: Bowman, Cindy G.

APPLICANT: Dawson, John L.

APPLICANT: Dunder, Erik M.

APPLICANT: Pace, Gary M.

APPLICANT: Suttie, Janet L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: CIBA-GRIGY Corporation

STREET: 7 Skyline Drive

CITY: Hawthorne

STATE: New York

COUNTRY: USA

ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30B

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/951,715A

FILING DATE: 25-SEP-1992

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Spruill, W. Murray

REGISTRATION NUMBER: 32,943

REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP

TELEPHONE: (919) 541-8615

TELEFAX: (919) 541-8689

INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..463
OTHER INFORMATION: /note= "protein sequence for
US-07-951-715A-25

Query Match 60.7%; Score 861.5; DB 1; Length 463;
Best Local Similarity 61.5%; Pred. No. 4.5e-80;
Matches 166; Conservative 36; Mismatches 67; Indels 1; Gaps 1;

QY 1 MANQTQ-ISKDYILGRLGEGFGITYLCTDRETRALACKSISKRLTAVDVVEDVRE 59
DB 2 LPQRTQNIREVYEVGRKLGQGFCTTCTRRASGKGFACKSIIPKRLCKEDYEDVWRE 61
QY 60 VTINSTLPEHPNVVVKLKYATYEDNETVHLVWELCEGGEFGIRIVARGHYTERAAATVARTI 119
DB 62 IQIMHHLSEHANVVRIGTYEDSTAVHLVWELCEGGEFGIRIVARGHYTERAAATVARTI 121
QY 120 AEVVRMCHVNGVWHRDLKPNFLPANKKENSALKAIIDFGLSVLPKPGERFTEIVGSPYYM 179
DB 122 VEVVEACHSLGVMHRDLKPNFLPANKKENSALKAIIDFGLSVLPKPGESFCDVVGSPYYV 181
QY 180 APEVLKRNYPGEVDVWSAGVILYLLCGVPPFWAETGQVALAILRGVLDKFRDPWSQIS 239
DB 182 APEVLKRLYGPESDVWSAGVILYLLSGVPPFWAETGQVALAILRGVLDKFRDPWSQIS 241
QY 240 ESAKSLVKQMLEPDSKRLTAQOVLDPHWI 269
DB 242 DSAKDLIRKMLDQNPKRLTAHEVLRHPWI 271

RESULT 11

US-08-459-448A-25
Sequence 25, Application US/08459448A
Patent No. 5859336

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESS: No. 585933artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,448A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..463
OTHER INFORMATION: /note= "protein sequence for
US-08-459-448A-25

Query Match 60.7%; Score 861.5; DB 2; Length 463;
Best Local Similarity 61.5%; Pred. No. 4.5e-80;
Matches 166; Conservative 36; Mismatches 67; Indels 1; Gaps 1;

QY 1 MANQTQ-ISKDYILGRLGEGFGITYLCTDRETRALACKSISKRLTAVDVVEDVRE 59
DB 2 LPQRTQNIREVYEVGRKLGQGFCTTCTRRASGKGFACKSIIPKRLCKEDYEDVWRE 61
QY 60 VTINSTLPEHPNVVVKLKYATYEDNETVHLVWELCEGGEFGIRIVARGHYTERAAATVARTI 119
DB 62 IQIMHHLSEHANVVRIGTYEDSTAVHLVWELCEGGEFGIRIVARGHYTERAAATVARTI 121
QY 120 AEVVRMCHVNGVWHRDLKPNFLPANKKENSALKAIIDFGLSVLPKPGERFTEIVGSPYYM 179
DB 122 VEVVEACHSLGVMHRDLKPNFLPANKKENSALKAIIDFGLSVLPKPGESFCDVVGSPYYV 181
QY 180 APEVLKRNYPGEVDVWSAGVILYLLCGVPPFWAETGQVALAILRGVLDKFRDPWSQIS 239
DB 182 APEVLKRLYGPESDVWSAGVILYLLSGVPPFWAETGQVALAILRGVLDKFRDPWSQIS 241
QY 240 ESAKSLVKQMLEPDSKRLTAQOVLDPHWI 269
DB 242 DSAKDLIRKMLDQNPKRLTAHEVLRHPWI 271

RESULT 12

US-08-459-595A-25
Sequence 25, Application US/08459595A
Patent No. 6018104

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.

APPLICANT: Wright, Martha S.
 APPLICANT: Merlin, Ellis J.
 APPLICANT: Launis, Karen L.
 APPLICANT: Rothstein, Steven J.
 APPLICANT: Bowman, Cindy G.
 APPLICANT: Dawson, John L.
 APPLICANT: Dunder, Erik M.
 APPLICANT: Pace, Gary M.
 APPLICANT: Suttie, Janet L.
 TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
 TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
 NUMBER OF SEQUENCES: 94
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 601810artis Corporation
 STREET: Patent & Trademark Dept., 520 White Plains
 STREET: Rd., POB 2005
 CITY: Tarrytown
 STATE: New York
 COUNTRY: USA
 ZIP: 10591-9005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/459,595A
 FILING DATE: 02-JUN-1995
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/951,715
 FILING DATE: 25-SEP-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/772,027
 FILING DATE: 04-OCT-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Pace, Gary M.
 REGISTRATION NUMBER: 40403
 REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919)541-8582
 TELEFAX: (919)541-8689
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 463 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..463
 OTHER INFORMATION: soybean CnpK as shown in Figure 34."
 /note= "protein sequence for

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QY 180 APEVLKRNVTGPEVDVWWSAGVILYLILCCGVPPFWAETEGGVALATILRGVL
DB 182 APEVLKRLKYGPESDVWWSAGVILYLILSGVPPFWAESPFGIFRQILLLGKLKD
QY 240 ESAKSLVKOMLEPDSKRLTLTAQOVLDPWI 269
DB 242 DSAKDLIRKWLDPNQPKRLTLTAHEVLRHPWI 271

RESULT 13
US-08-459-504B-25
; Sequence 25, Application US/08459504B
; Patent No. 6075185
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lytle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6075185artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,504B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/459,595
; FILING DATE: 02-JUN-1995
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 463 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FEATURE:

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; NAME/KEY: Protein
; LOCATION: 1..463
; OTHER INFORMATION: /note= "protein sequence for
; soybean CDPK as shown in Figure 34."
; US-08-459-504B-25

Query Match 60.7%; Score 861.5; DB 3; Length 463;
Best Local Similarity 61.5%; Pred. No. 4.5e-80;
Matches 166; Conservative 36; Mismatches 67; Indels 1; Gaps 1;

Qy 1 MANQTO-ISKYILGRLGRGEGITYLCTDRETREALACKSISKRLRTAVDVEDVRE 59
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 2 LPQRTQNIREVVEYVGRKLGQGFQGTTPCTTRASGKGFACKSIKPKLLCKEDYDVRE 61
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 60 VTINSTLPEHNVVVKLKYATYEDNETVHLVLMELCEGGEFGRIIVARGHYTERAAATVARTI 119
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 62 IQIMHHLSEHANVVRIEGTSTDAVHLVLMELCEGGEFGRIIVOKGHYSERQAARLTKTI 121
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 120 AEVVRMCHVNGVHRDLKPNFLFANKKENSALKKAIDFGLSVLPKPGERFTEIVGSPYIM 179
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 122 VEVVEACHSLGVHRDLKPNFLFDITDEDAKLKATDFGLSVFYKPGESFCDVVGSPYIV 181
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 180 APEVLKRNYPEDVMSAGVILYLLCGVPPFWAETEOGVVALAILRGVLDKFRDPWISOIS 239
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 182 APEVLKRLYGPESDVMSAGVILYLLSGVPPFWAESPFGIFRQILLGLKDFHSEWPSPIS 241
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 240 ESAKSLVKQMLEPDPSTKRLTAQOVLDPHWI 269
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 242 DSAKDLIRKMLDQNPKTRLTAEVLRHPWI 271
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
US-08-459-444-25
; Sequence 0, Application US/08459444
; Patent No. 6121014
; GENERAL INFORMATION:
; APPLICANT: Kozziel, Michael G.
; Desai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Launis, Karen L.
; TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
; NUCLEIC ACID CODING SEQUENCE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,444A
; FILING DATE: 02-Jun-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
```

```
; REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: /note= "protein sequence for
; soybean CDPK as shown in Figure 34."
; SEQUENCE CHARACTERISTICS:
; LENGTH: 463 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..463
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-08-459-444-25

Query Match 60.7%; Score 861.5; DB 3; Length 463;
Best Local Similarity 61.5%; Pred. No. 4.5e-80;
Matches 166; Conservative 36; Mismatches 67; Indels 1; Gaps 1;

Qy 1 MANQTO-ISKYILGRLGRGEGITYLCTDRETREALACKSISKRLRTAVDVEDVRE 59
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 2 LPQRTQNIREVVEYVGRKLGQGFQGTTPCTTRASGKGFACKSIKPKLLCKEDYDVRE 61
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 60 VTINSTLPEHNVVVKLKYATYEDNETVHLVLMELCEGGEFGRIIVARGHYTERAAATVARTI 119
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 62 IQIMHHLSEHANVVRIEGTSTDAVHLVLMELCEGGEFGRIIVOKGHYSERQAARLTKTI 121
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 120 AEVVRMCHVNGVHRDLKPNFLFANKKENSALKKAIDFGLSVLPKPGERFTEIVGSPYIM 179
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 122 VEVVEACHSLGVHRDLKPNFLFDITDEDAKLKATDFGLSVFYKPGESFCDVVGSPYIV 181
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Qy 180 APEVLKRNYPEDVMSAGVILYLLCGVPPFWAETEOGVVALAILRGVLDKFRDPWISOIS 239
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 182 APEVLKRLYGPESDVMSAGVILYLLSGVPPFWAESPFGIFRQILLGLKDFHSEWPSPIS 241
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 240 ESAKSLVKQMLEPDPSTKRLTAQOVLDPHWI 269
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 242 DSAKDLIRKMLDQNPKTRLTAEVLRHPWI 271
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
US-09-547-422-25
; Sequence 0, Application US/09547422
; Patent No. 6320100
; GENERAL INFORMATION:
; APPLICANT: Kozziel, Michael G.
; Desai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Launis, Karen L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6320100artis Agribusiness Biotechnology Research, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/547,422
; FILING DATE: 11-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/459,595
; FILING DATE: 02-JUN-1995
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-18805H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: /note= "protein sequence for
; soybean CDPK as shown in Figure 34."
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 463 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..463
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
;
; US-09-547-422-25

```

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Query Match      60.7%; Score 861.5; DB 3; Length 463;
Best Local Similarity 61.5%; Pred. No. 4.5e-80;
Matches 166; Conservative 36; Mismatches 67; Indels 1; Gaps 1;

QY      1  MANQTQ-ISKYILGRELGRGEGITYLCTDRETREALACKSISKRLRTAVDVEDVRR 59
Db      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY      2  LPQRTQNIREVYEVGRKLGQGGQGTTFECTRRASGGKGFACKSPKRLCKEDYDVWRE 61
Db      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY      60  VTIMSTLPEHPNVVVKLKATYEDNETVHLMELCEGGELFGRIVARGHYTERAAATVARTI 119
Db      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY      62  IQIMHLSHANVVRTEGTVEDSTAVHLMELCEGGELFDRIYQKHYSERQARLIKTI 121
Db      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY      120  AEVVRMCHVNGVMHRDLKPNFLFANKKENSALKAFDGLSVLFKPGERFTEIVGSPYYM 179
Db      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY      122  VEVVEACHSLGVNHRDLKPNFLFDITDEDAKLKATDFGLSVFYKPGESPCDVVGSFYV 181
Db      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY      180  APEVLKRNYPGVVDVNSAGVILYLLCGVPPFWAETEOGVVALAILRGVLDPKDPPWSQIS 239
Db      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
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QY      240  ESAKSLVKQMLEPDSKRLTAQQVLDHPWI 269
Db      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY      242  DSAKDLIRKMLDQNPKRLTAHEVLRHPWI 271
Db      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

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Search completed: October 14, 2005, 10:54:49
Job time : 22 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 14, 2005, 17:14:28 ; Search time 4656 Seconds
(without alignments)
2851.531 Million cell updates/sec

Title: US-08-989-881-2
Perfect score: 1419
Sequence: 1 MANQKISDYKYLGRG.....TKRLTAQVLDHPWQNAKK 274

Scoring table:

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Ygapop 10.0			0.5
Ygapop 6.0			7.0
Delop 6.0			7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2.1/USPTO.spool/US08989881/runat.14102005.112733.5182/app.query.fasta.1.455
-DB=GenEmbl -QFWT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=i -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US08989881 @CGN_1.1.4200 @runat.14102005.112733.5182 -NCPU=6 -ICPU=3
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-FCGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Database :

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2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1419	100.0	822	8	ATU73610
2	1395	98.3	1626	8	BT008900 Arabidops
3	1395	98.3	2044	8	AY140016 Arabidops
4	1322	93.2	1638	6	AX507164 Sequence

	5	1322	93.2	1638	6	AX651704
	6	1318	92.9	1638	8	BT004566 Arabidops
	7	1318	92.9	1842	8	ATHCDFKA
	8	1263	89.0	115721	8	F25A4
	9	1186	83.6	2313	8	AF276999
	10	1185.5	83.5	108767	8	AC011809 Arabidops
	11	1161	81.8	1617	6	CQ803946 Sequence
	12	1161	81.8	1617	8	BT012274 Arabidops
	13	1161	81.8	1700	8	BT011630
	14	1158	81.6	1967	6	AX077712 Sequence
	15	1158	81.6	1967	8	AF035944 Fragaria
	16	1142	80.5	1887	8	AJ699160 Nicotiana
	17	1141	80.4	1998	8	ATU31836
	18	1141	80.4	2115	8	AF316134 Arabidops
	19	1141	80.4	2368	8	AY138479 Caratopte
	20	1135	80.0	1884	8	BT003367 Arabidops
	21	1135	80.0	2086	8	AY062539 Arabidops
	22	1135	80.0	2087	6	AX077698 Sequence
	23	1135	80.0	2162	6	AX077694 Sequence
	24	1133	79.8	2366	8	AK068315 Oryza sat
	25	1132	79.8	1770	6	AX553371 Sequence
	26	1127	79.4	1602	6	AX507609 Sequence
	27	1127	79.4	1726	6	AX077695 Sequence
	28	1127	79.4	1896	6	ATU20624 Arabidops
	29	1124	79.2	1868	6	AX927170 Sequence
	30	1120	78.9	2205	8	BT013737 Lycopersi
	31	1115	78.6	1515	6	AX554091 Sequence
	32	1115	78.6	2252	8	AK066615 Oryza sat
	33	1106	77.9	2127	8	AK101942 Oryza sat
	34	1094	77.1	2163	8	AK105102 Oryza sat
	35	1041	73.4	2390	8	AK072981 Oryza sat
	36	1030	72.6	2216	8	AK117892 Arabidops
	37	1027	72.4	1892	6	AX537776 Sequence
	38	1011.5	71.3	1818	6	AX653174 Sequence
	C 39	997	70.3	90020	8	ATT24H18 Arabidops
	C 40	997	70.3	98506	8	ATT2L20 Arabidops
	41	985.5	69.5	91071	8	AC002339 Arabidops
	42	985.5	69.5	95824	8	U90439 Arabidops
	C 43	972.5	68.5	87503	8	ATT8H10 Arabidops
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ALIGNMENTS

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DEFINITION Arabidopsis thaliana ATCDPK1a (cpk1a) mRNA, partial cds.
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VERSION U73610.1 GI:502506
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SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
REFERENCE 1 (bases 1 to 822)
AUTHORS Sheen, J.
TITLE Ca2+-dependent protein kinases and stress signal transduction in plants
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 822)
AUTHORS Sheen, J.
TITLE Direct Submission
JOURNAL Submitted (08-OCT-1996) Department of Molecular Biology,
Massachusetts General Hospital, 50 Blossom Street, Boston, MA
02114, USA
Location/Qualifiers
1. 822
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/mol_type="mRNA"
/db_xref="taxon:3702"

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 /translation="MANQTQISDKYILGRLGRGFGITYLCTRETREALACKSISK
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ORIGIN

Alignment Scores:

Pred. No.: 1,266-134 Length: 822
 Score: 1419.00 Matches: 274
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 8 Gaps: 0

US-08-989-881-2 (1-274) x ATU73610 (1-822)

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 Db 1 ATGGCTAATCAAACTCAGTCAGCAGCAAGTACATCTTAGGACGAGAACTCGTCCGCGC 60
 Qy 21 GluPheGlyIleThrTyrLeuCysThrAspArgGluThrArgGluAlaLeuAlaCysIle 40
 Db 61 GAATTCGGAATCACGTATCTTTGTACAGATAGAGAGCTCGGAAGCTTTAGCTTGCAAA 120
 Qy 41 SerIleSerLysArgLysLeuArgThrAlaValAspValGluAspValArgGluVal 60
 Db 121 TCAATCTCCAGAGAAAGCTCCGAACCCGCTCGATGTGGAAGACGTCGTCGTGAAGTC 180
 Qy 61 ThrIleMetSerThrLeuProGluHisProAsnValValLysLeuLysAlaThrTyrGlu 80
 Db 181 ACGATCATGTCAACTTTACCGGAACACCCAAACGTTGTGAACCTTTAAAGCGCACTTATGAG 240
 Qy 81 AspAenGluThrValHisLeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArg 100
 Db 241 GATACAGAGACCGTCATCTTGTGATGAGCTTTGTGAAGGAGGTGAGCTTTTGTGCG 300
 Qy 101 IleValAlaArgGlyHisTyrThrGluArgAlaAlaThrValAlaArgThrIleAla 120
 Db 301 ATTGTTGCAAGAGGACATTATACAGAGCGTCGCGCGCTACCGTCGCGAGAACGATCGC 360
 Qy 121 GluValValArgMetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAen 140
 Db 361 GAAGTTGTGAGGATGTGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 420
 Qy 141 PheLeuPheAlaAsnLysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSer 160
 Db 421 TTCCTGTTTGTACACAGAGAGAAATTCGTCACCTTAAGGCTATTGATTTTGGTTTATCT 480
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 Db 481 GTTCTCTTTAAACCTGGAGAGAGGTTTACAGAGATTGTTGGAAGTCTTATTATATGCT 540
 Qy 181 ProGluValLeuLysArgAsnTyrGlyProGluValAspValTrpSerAlaGlyValIle 200
 Db 541 CCAGAAGTGTGTAAGAGAGAAATTTATGACACAGAGGTTGATGTGTGAGGTCTGGAGTTATC 600
 Qy 201 LeuTyrIleLeuLeuCysGlyValProProPheTyrAlaGluThrGluGlnGlyValAla 220
 Db 601 CTCACATCTTCTTGTGTTGTTCTCTCGTTTGGGACAGACCTGAACAGAGGTGTGCT 660
 Qy 221 LeuAlaIleLeuArgGlyValLeuAspPheLysArgAspProTyrSerGlnIleSerGlu 240
 Db 661 CTTGCGCATCTTGAGGGAGTCTTGTATTTTAAGAGAGATCTTGTGTCGAGATATCAGAG 720

Qy 241 SerAlaLysSerLeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAla 260
 Db 721 AGCGCAAAGAGCCTTGTGAAGCAGATGTTGAACCTGATTCAACTAAGCGTTGACTGCT 780
 Qy 261 GlnGlnValLeuAspHisProTyrIleGlnAenAlaLysLys 274
 Db 781 CAGCAAGTTCTTGATCATCCCTTGGATACAGATGCAAGAAAGAAA 822

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 VERSION BT008900.1 GI:31711965
 KEYWORDS FLI CDNA.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (bases 1 to 1626)
 Kim, C.J., Chen, H., Cheuk, R., Shinn, P., Bowser, L., Carninci, P.,
 Dale, J.M., Hayashizaki, Y., Iehida, J., Jones, T., Kamiya, A.,
 Karlin-Neumann, G., Kawai, J., Lam, B., Lin, J., Miranda, M.,
 Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L.,
 Sakurai, T., Satou, M., Seki, M., Southwick, A., Toriumi, M., Wong, C.,
 Wu, H.C., Yamada, K., Yu, G., Shinozaki, K., Davis, R.W., Theologis, A.
 and Ecker, J.R.
 Arabidopsis ORF clones
 Unpublished
 2 (bases 1 to 1626)
 Kim, C.J., Chen, H., Cheuk, R., Shinn, P., Bowser, L., Carninci, P.,
 Dale, J.M., Hayashizaki, Y., Iehida, J., Jones, T., Kamiya, A.,
 Karlin-Neumann, G., Kawai, J., Lam, B., Lin, J., Miranda, M.,
 Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L.,
 Sakurai, T., Satou, M., Seki, M., Southwick, A., Toriumi, M., Wong, C.,
 Wu, H.C., Yamada, K., Yu, G., Shinozaki, K., Davis, R.W., Theologis, A.
 and Ecker, J.R.
 Direct Submission
 Submitted (13-JUN-2003) Salk Institute Genomic Analysis Laboratory
 (SIGNAL), Plant Biology Laboratory, The Salk Institute for
 Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
 USA
 RIKEN Genomic Sciences Center (GSC) members carried out the
 collection and clustering of RAFL cDNAs (RAFL CDNA : 'RIKEN
 Arabidopsis Full-Length cDNA') : Seki, M., Narusaka, M., Iehida, J.,
 Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,
 Hayashizaki, Y. and Shinozaki, K.

TITLE
 JOURNAL
 REFERENCE
 AUTHORS

TITLE
 JOURNAL
 REFERENCE
 AUTHORS

COMMENT
 The Salk, Stanford, PGSC (SSP) Consortium members constructed and
 sequenced the pUNI (ORF) clones using the RAFL cDNAs: Kim, C.J.,
 Chen, H., Cheuk, R., Shinn, P., Bowser, L., Chan, M.M., Chang, C.M.,
 Dale, J.M., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J.,
 Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L.,
 Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K.,
 Yu, G., Davis, R.W., Theologis, A., and Ecker, J.R.

Kim, C.J. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to
 this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk)
 contributed equally to this work as PIs.

FEATURES
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DKRPMSQISSEKSLVKOMLEPDSFKELTAQOVLDPHPIQNAKKNAPGLDILVRS
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ORIGIN

Alignment Scores: 8.1e-132 Length: 1626
 Pred. No.: 1395.00 Matches: 269
 Score: 1395.00
 Percent Similarity: 99.27% Conservative: 3
 Best Local Similarity: 98.18% Mismatches: 2
 Query Match: 98.31% Indels: 0
 DB: 8 Gaps: 0

US-08-989-881-2 (1-274) x BT008900 (1-1626)

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Qy 21 GluPheGlyIleThrTyrLeuGlySerThrAspArgGluThrArgGluAlaLeuAlaCysLys 40
Dy 205 GAATTCGGAATCACGTATCTTTGTACAGATAGAGAGACTCGTGAAGCTTTAGCTGCAAA 264
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RESULT 3
LOCUS AY140016 2044 bp mRNA linear PLN 02-SEP-2002
DEFINITION Arabidopsis thaliana calcium-dependent protein kinase, putative
            (Atlg74740) mRNA, complete cds.
ACCESSION AY140016 GI:22655134
VERSION AY140016.1
KEYWORDS FLI CDNA.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1 (bases 1 to 2044)
AUTHORS Tripp,M., Southwick,A., Karlin-Neumann,G., Nguyen,M., Miranda,M.,
            Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H.,
            Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A.,
            Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K.,
            Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K.,
            Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.
TITLE Direct Submission
JOURNAL Submitted (12-AUG-2002) DNA Sequencing and Technology Center,
            Stanford University, 855 California Avenue, Palo Alto, CA 94304,
            USA
COMMENT e-mail for correspondence: arab@sequence.stanford.edu

RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
Arabidopsis Full-Length cDNA') : Seki,M., Narusaka,M., Ishida,J.,
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the
sequencing and annotation of the RAFL cDNAs: Tripp,M.,
Southwick,A., Nguyen,M., Palm,C.J., Jones,T., Wu,T., Chen,H.,
Cheuk,R., Chan,M.M., Chang,C.H., Dale,J.M., Deng,J.M., Hsuan,V.W.,
Lee,J.M., Kim,C.J., Quach,H.L., Shinn,P., Tang,C.C., Toroumi,M.,
Wallender,E.K., Wong,C., Wu,H.C., Yamada,K., Yu,G., Yuan,S.,
Ecker,J., Theologis,A. and Davis,R.W.

Tripp,M. (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed equally
to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W.
(SSP/Stanford) contributed equally to this work as PIs.

FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:

Pred. No.: 1,08e-131 Length: 2044
Score: 1395.00 Matches: 269
Percent Similarity: 99.27% Conservativity: 3
Best Local Similarity: 98.18% Mismatches: 2
Query Match: 98.31% Indels: 0
DB: 8 Gaps: 0

US-08-989-881-2 (1-274) x AY140016 (1-2044)

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RESULT 4

AX507164 1638 bp DNA linear PAT 27-SEP-2002
LOCUS Sequence 1859 from Patent WO0216655.
DEFINITION AX507164
ACCESSION AX507164
VERSION AX507164.1 GI:23388401
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopses.

REFERENCE

1 Harper, J.F., Kreps, J., Wang, X. and Zhu, T.
Stress-regulated genes of plants, transgenic plants containing
same, and methods of use
Patent: WO 0216655-A 1859 28-FEB-2002;
The Scripps Research Institute (US) ; Syngenta Participations AG
(CH)

FEATURES

source Location/Qualifiers
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Pred. No.: 2.13e-124 Length: 1638
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Best Local Similarity: 92.34% Mismatches: 13
Query Match: 93.16% Indels: 0
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Db 397 GATAACGAGAAAGCTGTCATCTGTTATGAGCTTTGTGAAGGAGGTGAGCTTTTGTATCGG 456
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LOCUS      AX651704
DEFINITION Sequence 533 from Patent WO03000898.
ACCESSION AX651704
VERSION    AX651704.1 GI:29154522
KEYWORDS   Arabidopsis thaliana (thale cress)
SOURCE     Arabidopsis thaliana
ORGANISM   Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
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REFERENCE 1
AUTHORS   Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M.,
          Katagiri, F., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. and Zou, G.
          Plant genes involved in defense against pathogens
          Patent: WO 03000898-A 533 03-JAN-2003;
          Syngenta Participations AG (CH)
FEATURES   Location/Qualifiers
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ORIGIN
Alignment Scores:
Pred. No.:      2,13e-124      Length:      1638
Score:          1322.00      Matches:     253
Percent Similarity: 95.26%      Conservative: 8
Best Local Similarity: 92.34%      Mismatches: 13
Query Match:     93.16%      Indels:      0
DB:              6              Gaps:        0

US-08-989-881-2 (1-274) x AX651704 (1-1638)

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Qy      21  GluPheGlyLeuThrTyriLeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLys 40
Db      217  GAATTCGGAATCACTTACCTCTGTACTGATCGTGAACCCAGCAGCTTTAGCTGCAAA 276
Qy      41  SerIleSerLysArgLysLeuArgThrAlaValAspValGluAspValArgGluVal 60
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Qy      61  ThrIleMetSerThrLeuProGluHisProAsnValValLysLeuLysLeuAlaThrTyriGlu 80
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Qy      141  PheLeuPheAlaAsnLysGluAsnSerAlaLeuLysAlaIleAaspPheGlyLeuSer 160
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Db      877  AGTGCAAGAGCTTGTGAGCAGAGATTGTGATCTGATCCGACTCAAGCGGTAACTGCT 936
Qy      261  GlnGlnValLeuAspHisProTrpIleGlnAsnAlaLysLys 274
Db      937  CAGCAAGTGTAGCTCACCATCGATACAGATGCAAGAA 978

RESULT 6
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DEFINITION Arabidopsis thaliana At1g18890 gene, complete cds.
ACCESSION BT004566
VERSION    BT004566.1 GI:28416562
KEYWORDS   FLI, CDNA.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 1638)
REFERENCE 1
AUTHORS   Cheuk, R., Chen, H., Kim, C.J., Shinn, P., Bowser, L., Carninci, P.,
          Chan, M.M., Chang, C.H., Dale, J.M., Hayashizaki, Y., Hsuan, V.W.,
          Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J.,
          Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M.,
          Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M.,
          Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K.,
          Yu, G., Yuan, S., Shinozaki, K., Davis, R.W., Theologis, A. and
          Ecker, J.R.
          Arabidopsis ORF clones
          Unpublished
          2 (bases 1 to 1638)
          Chan, R., Chen, H., Kim, C.J., Shinn, P., Bowser, L., Carninci, P.,
          Chan, M.M., Chang, C.H., Dale, J.M., Hayashizaki, Y., Hsuan, V.W.,
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          Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M.,
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          Yu, G., Yuan, S., Shinozaki, K., Davis, R.W., Theologis, A. and
          Ecker, J.R.
          Direct Submission
          Submitted (19-FEB-2003) Salk Institute Genomic Analysis Laboratory
          (SIGNAL), Plant Biology Laboratory, The Salk Institute for
          Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,

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primer_bind

polya_site

ORIGIN

Alignment Scores:

Pred. No.: 6.29e-124 Length: 1842
Score: 1318.00 Matches: 252
Percent Similarity: 94.89% Conservative: 8
Best Local Similarity: 94.97% Mismatches: 14
Query Match: 92.88% Indels: 0
DB: 8 Gaps: 0

US-08-989-881-2 (1-274) x ATHCDPKA (1-1842)

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DB 191 GAATTCGGAAATCACTTACCTCTGTACTGATCGTGAACCCAGAGCTTAGCTTGCACAA 250
QY 41 SerIleSerLysArgLysLeuArgThrAlaValAspValGluAspValArgGluVal 60
DB 251 TCGAATTCAGAGCAAGCTTCGAACAGCTGTCGATATCGAAGACGCTTCGTGCGAGGTA 310
QY 61 ThrIleMetSerThrLeuProGluHisProAsnValValLysLeuLysAlaThrTyrGlu 80
DB 311 GCGATTATGCTACTTTTACCTGAGCATCCAAACGCTAGTTAAGCTTAGTATGAG 370
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DB 371 GATACAGAGACGTCATCTGTTATGGAGCTTTGTGAAGGAGGTGAGCTTTTGTATCGG 430
QY 101 IleValAlaArgGlyHisTyrThrGluArgAlaAlaAlaThrValAlaArgThrIleAla 120
DB 431 ATTGTTGCTAGAGGACATTACAGGAGCGTCTGCTGCTGACGCTTTGCGAAGACGATTGCT 490
QY 121 GluValValArgMetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAsn 140
DB 491 GAGGTTGTGATGATGTGTCACCTCTAATGAGGTTATGTCATCGAGTTTGAACCTGAGAT 550
QY 141 PheLeuPheAlaAsnLysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSer 160
DB 551 TTCCTGTTGCTAAATAAAGAGGAAATCTCCACTAAGGCTATTGATTTTGGCTTGCT 610
QY 161 ValLeuPheLysProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAla 180
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QY 181 ProGluValLeuLysArgAsnTyrGlyProGluValAspValTrpSerAlaGlyValIle 200
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QY 221 LeuAlaIleLeuArgGlyValLeuAspPheLysArgAspProTrpSerGlnIleSerGlu 240
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DB 851 ACTGCCAAGAGCTTGTGAAGCAGATGTTGGATCTCTGATCCGACTAAGCGTTAACTGCT 910
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DB 911 CAGCAAGTGTAGCTCACCCATGGATACAGATGCAGAA 952
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DEFINITION sequence.
ACCESSION AC008263
VERSION AC008263.2 GI:5868932
KEYWORDS HTG.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 115721)
Vysotskaia,V.S., Schwartz,J.R., Yu,G., Toriumi,M., Lenz,C., Liu,S.,
Lee,J.M., Li,J., Gonzalez,A., Liu,A., Liu,K., Vaysberg,M.,
Sakano,H., Chin,C., Choi,E., Chio,J., Altafi,H., Araujo,R.,
Brooks,S., Buehler,E., Chao,Q., Conn,D., Conway,A.B., Dunn,P.,
Hansen,N., Hwang,B., Huizar,L., Khan,S., Kim,C., Palm,C.,
Rowley,D., Shinn,P., Walker,M., Davis,R.W., Ecker,J.R.,
Federspiel,N.A. and Theologis,A.
Arabidopsis thaliana chromosome 1 BAC F25A4 sequence
Unpublished
2 (bases 1 to 115721)
Theologis,A.
Direct Submission
Submitted (31-JUL-1999) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
3 (bases 1 to 115721)
Theologis,A.
Direct Submission
Submitted (10-SEP-1999) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
4 (bases 1 to 115721)
Theologis,A.
Direct Submission
Submitted (15-SEP-1999) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
COMMENT On Sep 10, 1999 this sequence version replaced gi:5668776.
The sequence of BAC F25A4 from Arabidopsis thaliana chromosome 1.
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gene
CDS

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Alignment Scores:

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Pred. No.:      4,36e-116      Length:      115721
Score:          1263.00      Matches:      267
Percent Similarity: 68.53%      Conservative: 3
Best local Similarity: 67.77%      Mismatches: 4
Query Match:      89.01%      Indels:      122
DB:              8          Gaps:        3

US-08-989-881-2 (1-274) x F25N4 (1-115721)

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QY 41 SerIleSerLysArgLysLeuArgThrAlaValAspValGluAspValArgArgGluVal 60
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QY 61 ThrIleMetSerThrLeuProGluHisProAsnValValLysLeuLysAlaThrTyrGlu 80
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QY 101 IleValAlaArgGlyHisTyrThrGluArgAlaAlaAlaThrValAlaArgThrIleAla 120
DB 92998 ATTGTTCAGAGAGCATATATACAGAGCGTGGCGGCTACCGTCCGAGAACGATCGCG 93057
QY 121 GluValValArgMetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAsn 140
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QY 141 PheLeuPheAlaAsnLysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSer 160
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QY 161 ValLeuPheLysPro----- 165
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QY 166 -----GlyGluArgPhe 169
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QY 210 ProPheTrpAla----- 213
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QY 214 -----GluThrGluGlnGlyValAlaLeuAla 222

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Db 93657 AAGAGCCTTGTGAAGCAGATGTTGAACCTGATTCAACTAAGCGTTTGTACTGCTCAGCA 93716
QY 263 ValLeu----- 264
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QY 264 ----- 264
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RESULT 9
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LOCUS Funaria hygrometrica calcium-dependent protein kinase gene, partial
DEFINITION cds.
ACCESSION AF276999
VERSION AF276999.1 GI:14484894
KEYWORDS Funaria hygrometrica
SOURCE Funaria hygrometrica
ORGANISM Funaria hygrometrica
REFERENCE 1 (bases 1 to 2313)
AUTHORS Mitra, D. and Johri, M.M.
TITLE Genomic DNA clone of a calcium-dependent protein kinase from the moss Funaria hygrometrica
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2313)
AUTHORS Mitra, D. and Johri, M.M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2000) Department of Biological Sciences, Tata Institute of Fundamental Research, Homi Bhabha Road, Mumbai, Maharashtra 400 005, India
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ORIGIN

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Alignment Scores:

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Pred. No.:      2,15e-110      Length:      2313
Score:          1186.00      Matches:      222
Percent Similarity: 88.56%      Conservative: 18

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Best Local Similarity:	81.92%	Mismatches:	31
Query Match:	83.56%	Indels:	0
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US-08-989-881-2 (1-274) x AF276999 (1-2313)			
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Db	157	ATCAGGTATTGTGCACGACAGCAAGAAACGACAGAGATTTTGTGCATCAAGTCTATATCT	216
Qy	44	LysArgLysLeuArgThrAlaValAspValGluAspValArgGluValThrIleMet	63
Db	217	AAGAAGAGCTCAGAACCGCGTGGATGTGGAGGATGTCCGGCGTGGAGTTGCCATTATG	276
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Db	757	CTAAGGGGGATACGGACTTCAAGAGGGATCCATGGCCGAAGGTGTCGGACTCGGCGAAG	816
Qy	244	SerLeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGlnGlnVal	263
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ORGANISM Arabidopsis thaliana			
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Unpublished			
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FEDERSPIEL, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altati, H., Nguyen, M., Lam, B., Southwick, A., Bei, Q., Buehler, E., Chin, C., Chio, J., Choi, E., Dunn, P., Gonzalez, A., Howing, B., Kim, C., Koo, T., Lee, J.M., Lenz, C., Li, J., Liu, A., Liu, K., Liu, S., Mukharsy, N., Pham, P., Sakano, H., Schwartz, J., Shinn, P., Thavari, A., Toriumi, M., Vayaberg, M., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.			
Direct Submission			
Submitted (15-OCT-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA			
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FEDERSPIEL, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altati, H., Araujo, R., Rowley, D., Buehler, E., Dunn, P., Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.			
Direct Submission			
Submitted (15-DEC-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA			
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FEDERSPIEL, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altati, H., Nguyen, M., Lam, B., Southwick, A., Ecker, J., Theologis, A. and Davis, R.W.			
Direct Submission			
Submitted (22-JAN-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA			
On Dec 15, 1999 this sequence version replaced gi:6041764.			
e-mail for correspondence: arab@sequence.stanford.edu			
Genes with similarity to proteins in the databases are described as 'putative', '-like' or 'similar to'. Genes that have EST similarity but no significant protein similarity are described as 'unknown proteins'. Genes that are annotated based only on gene prediction software are described as 'hypothetical proteins'. The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/section/index.html), GENSCAN (Chris Burge, http://gnomic.stanford.edu/~chris/GENSCANW.html), Fexa (V.Solovyev & A.Salamov, Sanger Centre, http://genomic.sanger.ac.uk/), and NetPlantGene (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/NetPlantGene.html).			
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VERSION CO803946.1 GI:47110607
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rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Inze,D., de Veylder,L. and Vlieghe,K.

IDENTIFICATION OF NOVEL e2f TARGET GENES AND USE THEREOF
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REFERENCE  1 (bases 1 to 1617)
AUTHORS   Cheuk,R., Chen,H., Kim,C.J., Shinn,P. and Ecker,J.R.
TITLE     Arabidopsis ORF clones
JOURNAL   Unpublished
REFERENCE  2 (bases 1 to 1617)
AUTHORS   Cheuk,R., Chen,H., Kim,C.J., Shinn,P. and Ecker,J.R.
TITLE     Direct Submission
JOURNAL   Submitted (27-MAR-2004) Salk Institute Genomic Analysis Laboratory
            (SIGnAL), Plant Biology Laboratory, The Salk Institute for
            Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
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Pred. No.: 4,766-108 Length: 1617
Score: 1161.00 Matches: 213
Percent Similarity: 88.43% Conservative: 24
Best Local Similarity: 79.48% Mismatches: 31
Query Match: 81.82% Indels: 0
DB: 8 Gaps: 0
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126 CysHisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsn 145
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592 AAGAAGGAGACTGCACCTCTTTAAGCGGATGATTTGGTCTCTCTGTTTCTTTAAACCA 651
166 GlyGluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluValLeuLys 185
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186 ArgAsnTyrGlyProGluValAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeu 205
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712 CGGAATATGCTCCAGAGTTGATATTTTGGAGTCAGGTGTAATTTCTTACATAGCTTA 771
206 CysGlyValProProPheThrAlaGluThrGluGlnGlyValAlaLeuAlaIleLeuArg 225
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772 TGTGCTGCTCCGCTTTCTGGCAGAACTGAAACAGAGGTTCACAAAGCAATTTATTGCA 831
226 GlyValLeuAspPheLysArgAspProTrpSerGlnIleSerGluSerAlaLysSerLeu 245
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952 CACCCGTGGTTACAGAAATGCAAG 975
BT011630 1700 bp mRNA linear PLN 28-FEB-2004
LOCUS      Arabidopsis thaliana At3g57530 mRNA, complete cds.
DEFINITION Arabidopsis thaliana (thale cress)
ACCESSION  BT011630
VERSION     BT011630.1 GI:44681391
KEYWORDS   FLI CDNA.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE  1 (bases 1 to 1700)
AUTHORS   Kim,C.J., Chen,H., Cheuk,R., Shinn,P. and Ecker,J.R.
TITLE     Arabidopsis cDNA clones
JOURNAL   Unpublished
REFERENCE  2 (bases 1 to 1700)
AUTHORS   Kim,C.J., Chen,H., Cheuk,R., Shinn,P. and Ecker,J.R.
TITLE     Direct Submission
JOURNAL   Submitted (28-FEB-2004) Salk Institute Genomic Analysis Laboratory
            (SIGnAL), Plant Biology Laboratory, The Salk Institute for
            Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
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CDS

ORIGIN

Alignment Scores:
Pred. No.: 5, 078-108 Length: 1700
Score: 1161.00 Matches: 213
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Best Local Similarity: 79.48% Mismatches: 31
Query Match: 81.82% Indels: 0
DB: 8 Gaps: 0

US-08-989-881-2 (1-274) x BT011630 (1-1700)

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Qy 46 LysLeuArgThrAlaValAspValGluAspValArgAspGluValThrIleMetSerThr 65
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LOCUS AX077712 Sequence 19 from Patent WO0107592.
DEFINITION AX077712
ACCESSION AX077712.1 GI:13122087
VERSION AX077712.1
KEYWORDS
SOURCE Fragaria x ananassa
ORGANISM Fragaria x ananassa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
REFERENCE 1
AUTHORS Holt, C.D., White, A.J., Michael, A.J. and Osborn, R.W.
TITLE Herbicide resistant plants and methods for the production thereof
JOURNAL Patent: WO 0107592-A 19 01-FEB-2001;
ZENECA LIMITED (GB)
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 ACCESSION AF035944
 VERSION
 KEYWORDS
 SOURCE Fragaria x ananassa
 ORGANISM
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
 1 (bases 1 to 1967)
 Llop-Tous, I., Dominguez-Puigjaner, E. and Vendrell, M.
 Direct Submission
 Submitted (26-NOV-1997) Agrobiologia, CSIC, Jordi Girona 18-26, Barcelona 08034, Spain
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polyA_site

ORIGIN

Alignment Scores:
 Pred. No.: 1-23e-107 Length: 1967
 Score: 1158.00 Matches: 215
 Percent Similarity: 88.89% Conservative: 25
 Best Local Similarity: 79.63% Mismatches: 30
 Query Match: 81.61% Indels: 0
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US-08-989-881-2 (1-274) x AF035944 (1-1967)

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 QY 145 AsnLysLysGluAsnSerAlaLeuLysAlaLeuAspPheGlyLeuSerValLeuPheLys 164
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 QY 165 ProGlyGluArgPheThrGluLeuValGlySerProTyrTyrMetAlaProGluValLeu 184
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Job time : 4760 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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Run on: October 14, 2005, 17:11:37 ; Search time 588 Seconds
(without alignment)
2758.519 Million cell updates/sec

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Perfect score: 1419
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Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : N Geneseq_16Dec04: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	1322	93.2	1638	8	ADA68553 Arabidops
5	1161	81.8	1617	12	ADN72462 Thale cre

6	1161	81.8	1836	3	AAC47633 Arabidops
7	1158	81.6	1967	4	AAF74280 Strawberry
8	1135	80.0	2087	4	AAF74266 Arabidops
9	1135	80.0	2162	4	AAF74262 Arabidops
10	1132	79.8	1770	8	ADA69918 Rice gene
11	1132	79.8	1770	12	ADJ39574 Plant cDN
12	1127	79.4	1602	6	AB214499 Arabidops
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14	1124	79.2	1868	10	ADF38032 Synchroni
15	1115	78.6	1515	8	ADA70638 Rice gene
16	1071	75.5	960	12	ADA744509 Plant cDN
17	1027	72.4	1692	8	ADA70323 Rice gene
18	1011.5	71.3	1818	8	ADA69721 Rice gene
19	970	68.4	912	12	ADJ42517 Plant cDN
20	957	67.4	1647	4	AAF74281 Liverwort
21	957	67.4	1647	4	AAF74282 Arabidops
22	947	66.7	2230	6	ABA91081 Physcomit
23	930	65.5	690	10	ADC08881 Corn DNA
24	930	65.5	690	12	ADJ44765 Plant cDN
25	930	65.5	1797	8	ADA71210 Rice gene
26	929	65.5	1392	3	AAC48741 Arabidops
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28	916	64.6	1833	6	AB214529 Arabidops
29	916	64.6	1839	8	ADA71195 Rice gene
30	907	63.9	1719	8	ADA70078 Rice gene
31	903	63.6	3054	3	AAC45753 Arabidops
32	900	63.4	1133	4	AAC85833 Tobacco h
33	899	63.4	2550	4	AAF74283 Cucurbita
34	898	63.3	2439	8	ADA70481 Rice gene
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37	893	62.9	2040	4	AAF74278 Rice calc
38	891	62.8	1782	8	ADA71107 Rice gene
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42	887	62.5	1747	6	ABA06021 Arabidops
43	887	62.5	1761	3	AAC42353 Arabidops
44	887	62.5	2306	4	AAF74272 Maize cal
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ALIGNMENTS

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XX
DT 27-AUG-2003 (revised)
DT 12-OCT-1998 (first entry)
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DE Nucleotide sequence of ATCDPK1a PK domain.
XX
KW ATCDPK1a; protein kinase; PK; tolerance; drought; salinity; cold; heat;
KW fruit; ornamental; vegetable; cereal; field crops; ds.
XX
OS Arabidopsis sp.
XX
FH Key Location/Qualifiers
CDS 97..918
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FT /product= "ATCDPK1a PK protein"
FT /note= "no stop codon specified"

XX	PN	WO9826045-A1.
XX	PD	18-JUN-1998.
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PF	12-DEC-1997;	97WO-US023019.
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PR	13-DEC-1996;	96US-0032966P.

XX (GEHO) GEN HOSPITAL CORP.
 PA Sheen J;
 XX WPI; 1998-348509/30.
 DR P-PSDB; AAW49837.
 XX
 PT Protecting plants against environmental stress - by introducing protein
 PT kinase domain-containing gene, calcium dependent protein kinase gene or
 PT calcium/calmodulin-dependent gene.
 XX
 PS Claim 17; Fig 5; 62pp; English.
 XX
 CC This is the nucleotide sequence of the ATCDPK1a protein kinase (PK)
 CC domain isolated from the Arabidopsis cDNA library, and used in the method
 CC of the invention to protect plants against environmental stress. The
 CC methods can be used for improving the tolerance of plants to
 CC environmental stresses such as drought, salinity, cold and heat. They
 CC provide for increased production efficiency, as well as for improvements
 CC in quality and the yield of crop plants and ornamentals. The methods
 CC contribute to the production of high quality and high yield agricultural
 CC products, e.g. fruits, ornamentals, vegetables, cereals, and field crops.
 CC (Updated on 27-AUG-2003 to correct OS field.)
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Alignment Scores:
 Pred. No.: 4,35e-155 Length: 1020
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 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-08-989-881-2 (1-274) x AAV36878 (1-1020)

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 Qy 21 GluPheGlyIleThrTyrLeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLys 40
 Db 157 GAATTCGGAATCAGTATCTTTGACAGATAGAGAGACTCGTAGGCTTTAGCTTGCAA 216
 Qy 41 SerIleSerLysArgLysLeuArgThrAlaValAspValGluAspValArgGluVal 60
 Db 217 TCAATCTCCAAGAGAAAGCTCCGAACCGCGTCGATGTGGAAGACGTCCTCGTGAATC 276
 Qy 61 ThrIleMetSerThrLeuProGluHisProAsnValLysLeuLysAlaThrTyrGlu 80
 Db 277 ACGATCATGTCAACTTTACCGGAACACCCCAACGTTGTGAACCTTAAAGCGACTTTATGAG 336
 Qy 81 AspAsnGluThrValHisLeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArg 100
 Db 337 GATAACGAGACCGTGCATCTTTGTGAGGACCTTTGTGAAGGAGTGAGCTTTTGTGCG 396
 Qy 101 IleValAlaArgGlyHisTyrThrGluArgAlaAlaThrValAlaArgThrIleAla 120
 Db 397 ATTGTTGCAAGAGAGACATTATACAGAGCGTGCAGCGCTACCGTCGCGAAGCATCGCG 456
 Qy 121 GluValValArgMetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAsn 140
 Db 457 GAAGTTGTGAGGATGTCTATGTCAATGTGTTATGATAGAGATTGGAAGCTTGAGAT 516
 Qy 141 PheLeuPheAlaAsnLysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSer 160
 Db 517 TTCTTGTTTCTAACAAGAGAGAAATTCGCACCTTAAGGCTATTGATTGTGTTATCT 576
 Qy 161 ValLeuPheLysProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAla 180
 Db 577 GTTCTCTTTAAACCTGGAGAGAGGTTTACAGAGATTGTTGGAAGTCTCTATTATATGCGCT 636

Qy 181 ProGluValLeuLysArgAsnTyrGlyProGluValAspValTyrSerAlaGlyValIle 200
 Db 637 CCAGAAAGTGTGAAGAGAAATATGACCAGAGGTTGATGTGTGGAGTCTGCTGGAGTATC 696
 Qy 201 LeuTyrIleLeuLeuCysGlyValProProPheTyrAlaGluThrGluGlnGlyValAla 220
 Db 697 CTCACATCTTCTTGTGTGTTCTCTCGTCTTGGCGAGAGACTGCAACAAGGTGTGGCT 756
 Qy 221 LeuAlaIleLeuArgGlyValLeuAspPheLysArgAspProTyrSerGlnIleSerGlu 240
 Db 757 CTTGCCATCTTGAAGGAGTCTTCTGATTTTAAAGAGAGATCCTTGGTCCGAGATATCAGAG 816
 Qy 241 SerAlaLysSerLeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAla 260
 Db 817 ACGCAAGAGCGCTTGTGAAGCAGATGTTGGAACTGATTCACCTAAGCGTTTGAAGTCT 876
 Qy 261 GlnGlnValLeuAspHisProTyrIleGlnAsnAlaLysLys 274
 Db 877 CAGCAAGTTCTTGTATCACCCTTGGATACAGATGCAAGTGAAGTCTTGAAGTCTTGAAGTCT 918

RESULT 2
 AAI66819
 ID AAI66819 standard; DNA; 1020 BP.
 XX
 AC AAI66819;
 XX
 DT 07-JAN-2002 (first entry)
 XX
 DE ATCDPK1a PK domain nucleotide sequence.
 XX
 KW Plant protoplast; gene expression; Arabidopsis; PK; CDPK; ATCDPK1a;
 KW calcium activated protein kinase; calcium dependant protein kinase; ds.
 XX
 OS Arabidopsis thaliana.
 XX
 FH Key Location/Qualifiers
 FT CDS 97..918
 FT /*tag= a
 XX
 PN WO200169920-A1.
 XX
 PD 20-SEP-2001.
 XX
 PF 13-MAR-2001; 2001WO-US007999.
 XX
 PR 13-MAR-2000; 2000US-0189074P.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 PI Sheen J;
 XX
 XX WPI; 2001-611395/70.
 DR P-PSDB; AAG65759.
 XX
 PT Using plant protoplast expression systems for rapidly screening libraries
 PT of nucleic acids to identify gene that modulate expression of target
 PT genes.
 XX
 PS Example; Fig 5A-C; 95pp; English.
 XX
 CC The invention provides a high through-put assay for rapidly screening a
 CC library of nucleic acid molecules to identify a gene product that
 CC modulates expression of a gene of interest in plant protoplasts. The
 CC method comprises: (1) introducing into 1 or more plant protoplasts: (a) a
 CC reporter gene construct operably linked to a promoter of a gene of
 CC interest; and (b) a member of a library of nucleic acid molecules (the
 CC library member is expressed in the plant protoplasts); and (2) screening
 CC the protoplasts to determine whether the amount of gene expression of the
 CC reporter gene construct changes in response to the expression of the
 CC library members, a change in gene expression of the reporter gene
 CC construct identifying the gene product expressed by the library member as
 CC 1 that modulates expression of the gene of interest. The present sequence
 CC represents the nucleotide sequence of Arabidopsis calcium dependant

CC	protein kinase (CDPK) ATCDPK1a PK domain	
XX	Sequence 1020 BP; 265 A; 194 C; 280 G; 277 T; 0 U; 4 Other;	
SQ		
Alignment Scores:		
Pred. No.:	4,35e-155	Length: 1020
Score:	1419.00	Matches: 274
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DB:	4	Gaps: 0
US-08-989-881-2 (1-274) x AA166819 (1-1020)		
Qy	1 MetAlaAsnGlnThrGlnIleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGly 20	
Db	97 ATGGCTAATCAAACTCAGATCAGCGACAAAGTACATCTTTAGGACGAGAACTCGGTGCGGCG 156	
Qy	21 GluPheGlyIleThrTyrLeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLys 40	
Db	157 GAATTCCGAATCAGGTATCTTTGTACAGATAGAGACTCGTGAAGCTTTAGCTTGCANA 216	
Qy	41 SerIleSerLysArgLysLeuArgThrAlaValAspValGluAspValArgGluVal 60	
Db	217 TCAATCTCCAAGAGAAAGCTCCGAACCGCGTCGATGTGGAAGAGCTCCGTCGTGAAGTC 276	
Qy	61 ThrIleMetSerThrLeuProGluHisProAsnValValLysLeuLysAlaThrTyrGlu 80	
Db	277 ACGATCATGTCAACTTTACCGGAACACCCAAACGTTGTGAACCTTTAAAGCGACTTATGAG 336	
Qy	81 AspAsnGluThrValHisLeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArg 100	
Db	337 GATAACGAGACCGTCATCTTGTGATGAGCTTTGTGAAGGAGGTGAGCTTTTGGTGGG 396	
Qy	101 IleValAlaArgGlyHisTyrThrGluArgAlaAlaThrValAlaArgThrIleAla 120	
Db	397 ATTGTGCAAGAGACATTATACAGAGCGTGGCGGCTACCGTCGCGAGAACGATCGG 456	
Qy	121 GluValValArgMetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAsn 140	
Db	457 GAAGTTGTGAGAGATGTGTCATGTCAATGGTGTATATGCATAGAGATTTGAAGCCTGAGAAT 516	
Qy	141 PheLeuPheAlaAsnLysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSer 160	
Db	517 TTCCTGTTTGTCTAACAGAGAGAAATTCGCACCTTAAGGCTATTGATTTTGGTTTATCT 576	
Qy	161 ValLeuPheLysProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAla 180	
Db	577 GTTCTCTTTAAACCTGGAGAGAGGTTTACAGAGATTGTGGAAGTCTTATTATATGGCT 636	
Qy	181 ProGluValLeuLysArgAsnTyrGlyProGluValAspValTrpSerAlaGlyValIle 200	
Db	637 CCAGAAGTGTGTAAGAGAGAAATTTATGACACAGAGGTTGATGTGTGGAGTGCTGGAGTTATC 696	
Qy	201 LeuTyrIleLeuLeuCysGlyValProPheTrpAlaGluThrGluGlnGlyValAla 220	
Db	697 CTCACATCTTCTTTGTGGTGTCTCCCTCGTTTGGCGAGAGACTGAACAAGGTGTGGCT 756	
Qy	221 LeuAlaIleLeuArgGlyValLeuAspPheLysArgAspProTrpSerGlnIleSerGlu 240	
Db	757 CTTCGCCATCTTGAGGGGAGTCTTGTGATTTTAAGAGAGATCCTTGGTCGACATATCAGAG 816	
Qy	241 SerAlaLysSerLeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAla 260	
Db	817 AGCCCAAGAGCCCTTGTGAAGCAGATGTTGAACCTGATTCACACTAAGCGTTTGAAGTCT 876	
Qy	261 GlnGlnValLeuAspHisProTyrIleGlnAsnAlaLysLys 274	
Db	877 CAGCAAGTCTTGTATCACCCTTGGATACAGAAATGCCAAGAAA 918	
RESULT 3		
ABZ14054		
ID	ABZ14054 standard; DNA; 1638 BP.	

XX	ABZ14054;	
AC		
XX	21-JAN-2003 (first entry)	
DT		
XX	Arabidopsis thaliana stress regulated gene SEQ ID NO 1859.	
DE		
XX	Arabidopsis thaliana; plant; gene; stress; transgenic; da.	
KW		
XX	Arabidopsis thaliana.	
OS		
XX	Arabidopsis thaliana.	
FN	WO200216655-A2.	
XX		
PD	28-FEB-2002.	
XX		
PF	24-AUG-2001; 2001WO-US026685.	
XX		
PR	24-AUG-2000; 2000US-0227866P.	
PR	26-JAN-2001; 2001US-0264647P.	
PR	22-JUN-2001; 2001US-0300111P.	
XX	(SCRI) SCRIPPS RES INST.	
PA	(SYGN) SYNGENTA PARTICIPATIONS AG.	
PA		
XX	Harper JF, Kreps J, Wang X, Zhu T;	
PI		
XX	WPI; 2002-304127/34.	
DR		
XX	Identifying a stress condition to which a plant cell has been exposed and	
PT	producing plants with increased tolerance to these abiotic stresses.	
PT		
XX	Claim 144; SEQ ID NO 1859; 577bp + Sequence Listing; English.	
PS		
XX	The invention relates to identifying a stress condition to which a plant	
CC	cell has been exposed, comprising: (a) contacting nucleic acid	
CC	representative of expressed polynucleotides in the plant cell with an	
CC	array or probes representative of the plant cell genome; and (b)	
CC	detecting a profile of expressed polynucleotides in the plant cell	
CC	characteristic of a stress response. The method is useful in the	
CC	production of transgenic plants, cells and seeds and in producing plants	
CC	with increased tolerance to abiotic stress. The present sequence is that	
CC	of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used	
CC	in methods of the invention. Note: The sequence data for this patent is	
CC	not represented in the printed specification but is based on sequence	
CC	information supplied to Derwent by the European Patent Office	
XX		
SQ	Sequence 1638 BP; 482 A; 291 C; 416 G; 449 T; 0 U; 0 Other;	
Alignment Scores:		
Pred. No.:	1.67e-143	Length: 1638
Score:	1322.00	Matches: 253
Percent Similarity:	95.26%	Conservative: 8
Best Local Similarity:	92.34%	Mismatches: 13
Query Match:	93.16%	Indels: 0
DB:	6	Gaps: 0
US-08-989-881-2 (1-274) x ABZ14054 (1-1638)		
Qy	1 MetAlaAsnGlnThrGlnIleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGly 20	
Db	157 ATGAGCAATCAAACTCAGATCAGCGACAAATACATCTTAGTCTCGTAATTAGTTCGAGGC 216	
Qy	21 GluPheGlyIleThrTyrLeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLys 40	
Db	217 GAATTCGGAATCACTTACCTCTGTACTGATCGTGAACCCACGAAAGCTTTAGCTTGCANA 276	
Qy	41 SerIleSerLysArgLysLeuArgThrAlaValAspValGluAspValArgGluVal 60	
Db	277 TCGATTTCAAGCGAAGACCTTCGNACAGCTTCGATATCGNAGACGTTCTGTCGTGAGTA 336	
Qy	61 ThrIleMetSerThrLeuProGluHisProAsnValValLysLeuLysAlaThrTyrGlu 80	
Db	337 GCGATTATGCTACTTTTACCTGAGCATCCAAACGCTAGCTTAAGCTTAAGGCTTAGTTATGAG 396	

Qy	81	AspAsnGluThrValHisLeuValMetGluLeuCysGluGlyGluLeuPheGlyArg	100
Db	397	GATAACGAGAACTGCATCTGGTTATGGAGCTTTGTGAAGGAGGTGAGCTTTTGTGATCGG	456
Qy	101	IleValAlaArgGlyHisTyrThrGluArgAlaAlaAlaThrValAlaArgThrIleAla	120
Db	457	ATTGTTGCTAGAGGACATTACACGAGGCGTGCTGCGAGCTGTTCGGAAGACGATTGCT	516
Qy	121	GluValValArgMetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAsn	140
Db	517	GAGTTTGATGATGTGTGCACCTCTAATGGAGTTATGCATCGAGATTGGAACCTGAGAA	576
Qy	141	PheLeuPheAlaAsnLysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSer	160
Db	577	TTCITGTTTCTAATAAAAGGAGAATCTCCACTAAAGGCTATTGATTTTGGCTTGCT	636
Qy	161	ValLeuPheLysProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAla	180
Db	637	GTGTTCTTCAAACCTGGAGATAAGTTACAGAGATTGTAGGAAGTCCGTATTATATGGCT	696
Qy	181	ProGluValLeuLysArgAsnTyrGlyProGluValAspValTrpSerAlaGlyValIle	200
Db	697	CCAGAAGTGTTGAAGAGAGATTATGACCAGGGGTTGATGTGTGGAGTCCCGAGGTATT	756
Qy	201	LeuTyrIleLeuLeuCysGlyValProPheTrpAlaGluThrGluGlnGlyValAla	220
Db	757	ATCTATATCTTGCTCTGTGGTGTTCTCCGTTTTGGGCTGAGACTGAACAAGGTGTGCT	816
Qy	221	LeuAlaIleLeuArgGlyValLeuAspPheLysArgAspProTrpSerGlnIleSerGlu	240
Db	817	CTTGGGATCTTGGGGGAGTCTTGATTTTAAGAGAGACCCCTTGGCCTCAGATATCAGAG	876
Qy	241	SerAlaLysSerLeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAla	260
Db	877	AGTGCCAAGAGCCTTGTGAAGCAGATGTTGGATCCTGATCCGACTAAGCGGTTAACTGCT	936
Qy	261	GlnGlnValLeuAspHisProTrpIleGlnAsnAlaLysLys	274
Db	937	CAGCAAGTGTTAGCTTCACCCATGGATACAGAAATGCAAGAAA	978

RESULT 4

ADA68553	standard; DNA; 1638 BP.
ADA68553;	
20-NOV-2003	(first entry)
Arabidopsis thaliana gene, SEQ ID 533.	
Plant; bacterial infection; fungal infection; viral infection; ds.	
Arabidopsis thaliana.	
WO2003000898-A1.	
03-JAN-2003.	
22-JUN-2001; 2001WO-IB001105.	
22-JUN-2001; 2001WO-IB001105.	
(SYGN) SYNGENTA PARTICIPATIONS AG.	
Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y, Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G; WPI; 2003-175290/17.	
Identifying at least one gene involved in plant resistance or response to pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant	

gene expression.

Claim 6; SEQ ID NO 533; 899pp; English.

The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.

Sequence 1638 BP; 482 A; 291 C; 416 G; 449 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.67e-143	Length:	1638
Score:	1322.00	Matches:	253
Percent Similarity:	95.26%	Conservative:	8
Best Local Similarity:	92.34%	Mismatches:	13
Query Match:	93.16%	Indels:	0
DB:	8	Gaps:	0

US-08-989-881-2 (1-274) x ADA68553 (1-1638)

Qy	1	MetAlaAsnGlnThrGlnIleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGly	20
Db	157	ATGAGCAATCAAACTCAGATCAGCGACAAATACATCTTAGTTCGTGAATTAGTCTGAGGC	216
Qy	21	GluPheGlyIleThrTyrLeuCytsThrAspArgGluThrArgGluAlaLeuAlaCyLys	40
Db	217	GAATTCGGAATCACTTACCTCTGTACTGATCGTGAAACCCACGAAGCTTTAGCTTGC	276
Qy	41	SerIleSerLysArgLysLeuArgThrAlaValAspValGluAspValArgGluVal	60
Db	277	TCGATTTCAAAGCGAAGGCTTCGAACAGCTGTCGATATCGAAGACGTTCTGTCGAGGTA	336
Qy	61	ThrIleMetSerThrLeuProGluHisProAsnValValLysLeuLysAlaThrTyrGlu	80
Db	337	GCGATTATGTCTACTTTACTGTGAGCATCCAAAGTAGTTAAGCTTAAGGCTAGTTATGAG	396
Qy	81	AspAsnGluThrValHisLeuValMetGluLeuCytsGluGlyGluLeuPheGlyArg	100
Db	397	GATAACGAGAACGTCGATCTGGTTATGGAGCTTGTGAAGGAGGTGAGCTTTTGATCGG	456
Qy	101	IleValAlaArgGlyHisTyrThrGluArgAlaAlaAlaThrValAlaArgThrIleAla	120
Db	457	ATTGTTGCTAGAGGACATTACACGAGGCGTGTCTGTCGAGCTGTTCCGAGAACGATTGCT	516
Qy	121	GluValValArgMetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAsn	140
Db	517	GAGGTTGTGATGATGTGTCACCTCTAATGCGATTATGATCGAGATTTGAAACCTGAGAAT	576
Qy	141	PheLeuPheAlaAsnLysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSer	160
Db	577	TTCTCTGTTTGCCTAATAAAGAGAGAAATCTCCACATAAAGGCTATTGATTTGGCTTGTCT	636
Qy	161	ValLeuPheLysProGlyGluPheThrGluIleValGlySerProTyrTyrMetAla	180
Db	637	GTGTTCTTCAAACCTGGAGATAAGTTTACAGAGATTGTAGGAAGTCCGTTATATATGGCT	696
Qy	181	ProGluValLeuLysArgAsnTyrGlyProGluValAspValTrpSerAlaGlyValIle	200
Db	697	CCAGAAAGTGTGAAGAGAGATTATGGACCACGGGGTTGATGTGGAGTCCCGAGTTATT	756
Qy	201	LeuTyrIleLeuLeuCytsGlyValProPheThrAlaGluThrCluGlnGlyValAla	220
Db	757	ATCTATATCTGCTCTGTGGGTGTTCTCCGTTTTGGGCTGAGACTGAACAGGTGTGCT	816
Qy	221	LeuAlaIleLeuArgGlyValLeuAspPheLysArgAspProTrpSerGlnIleSerGlu	240

Db 817 CTTCGATCTTCGGGGAGTCTTGATTTTAAGAGAGACCCTTGGCCTCAGATATCAGAG 876
 Qy 241 SerAlaLysSerLeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAla 260
 Db 877 AGTGCACAGAGCTTGTGAAGCAGATGTTGGATCTCGATCCGACGATTAAGCGTTAACTGCT 936

Qy 261 GlnGlnValLeuAspHisProTyrPileGlnAsnAlaLysLys 274
 Db 937 CAGCAGGTGTTAGCTCACCCATGGATACAGAAATGCAAGAA 978

RESULT 5

ADN72462
 ID ADN72462 standard; cDNA; 1617 BP.

XX AC ADN72462;

XX DT 15-JUL-2004 (first entry)

XX DE Thale cress cDNA upregulated in E2Fa/Dpa expressing plants SeqID 357.

XX KW gene; ss; plant; transgenic; E2Fa/Dpa transcription factor;

XX KW growth regulator; animal feed product; thale cress;

XX KW cell wall biosynthesis; nitrogen metabolism; carbon metabolism.

XX OS Arabidopsis thaliana.

XX PN WO2004035798-A2.

XX PD 29-APR-2004.

XX PF 20-OCT-2003; 2003WO-EP011658.

XX PR 18-OCT-2002; 2002EP-00079408.

XX PA (CROP-) CROPDESIGN NV.

XX PI Inze D, De Veylder L, Vlieghe K;

XX DR WPI; 2004-348466/32.

XX DR P-PSDB; ADN72463.

PT Altering plant characteristics, useful for producing plants for enzyme or pharmaceutical production comprises modifying in a plant, expression of one or more nucleic acids and/or modifying level or activity of one or more proteins.

XX PS Claim 1; SEQ ID NO 357; 134pp; English.

XX CC This invention relates to a novel method for altering one or more plant characteristics. Specifically, it refers to identifying genes that are up- or down-regulated in transgenic plants overexpressing the heterodimeric E2Fa/Dpa transcription factor of Arabidopsis and using these sequences to alter plant characteristics accordingly. The present invention describes generating transgenic plants for the production of growth regulators, enzymes, therapeutics, pharmaceuticals and animal feed products, where the altered plant characteristics are selected from increased yield or biomass, enhanced survival capacity, stress tolerance, plant architecture or physiology, altered endoreplication, biochemistry, signal transduction, storage lipid mobilisation and/or altered photosynthesis, each relative to the corresponding wild type plants. Accordingly, these sequences can also be useful as positive or negative selectable markers during transformation of cells or tissues. The identified genes play a role in a variety of biological processes such as DNA replication, cell wall biosynthesis, nitrogen and/or carbon metabolism or they function as transcription factors. This polynucleotide sequence is thale cress cDNA upregulated 1.3 fold or more in plants overexpressing the E2Fa/Dpa transcription factor, given in an exemplification of the invention.

SQ Sequence 1617 BP; 499 A; 271 C; 430 G; 417 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9.16e-125 Length: 1617
 Score: 1161.00 Matches: 213

Percent Similarity: 88.43% Conservative: 24
 Best Local Similarity: 79.48% Mismatches: 31
 Query Match: 81.82% Indels: 0
 DB: 12 Gaps: 0

US-08-989-881-2 (1-274) x ADN72462 (1-1617)

Qy 6 GlnIleSerAspLysTyrIleLeuGlyArgGluLeuGlyGluPheGlyIleThr 25
 Db 172 GAGATCGAGTCTAAATACACGTTGGGAGAGAGCTAGGTCTGGAGAAATTCGGTTCAGG 231

Qy 26 TyrLeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerLysArg 45
 Db 232 TATCTATGTACTGATAAGGACAGACGACGCTTTTGTCTGTAATCCATTTGAGGAAG 291

Qy 46 LysLeuArgThrAlaValAspValGluAspValArgGluValThrIleMetSerThr 65
 Db 292 AAGCTGAGGACAGCTGTTGATATTGAAGATCTTAGGAGAGAGGTTGAGATTATGAGCAT 351

Qy 66 LeuProGluHisProAsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrVal 85
 Db 352 ATGCTCAGCATCTCTAATGTTGTTTACTTTTGAAGGAGACTTATGAGGATGAGCATGCTGT 411

Qy 86 HisLeuValMetGluLeuCysGluGlyGluLeuPheGlyArgIleValAlaArgGly 105
 Db 412 CATTTGGTTATGGAGCTTTGTGAAGGTGGTGAATTTGTTGATGAGATTGTTGCTAGAGG 471

Qy 106 HisTyrThrGluArgAlaAlaAlaThrValAlaAlaArgThrIleAlaGluValValArgMet 125
 Db 472 CATTATATGAGAGAGCTGCTGCTGTCTCATAAGACCATCATGGAAGTTGTTCCAGGTG 531

Qy 126 CysHisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsn 145
 Db 532 TGTCTAATAGCATGGGGTAATGCACAGGGACCTGAAACCTGAGAACTCTCTGTTGGAAAC 591

Qy 146 LysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysPro 165
 Db 592 AAGAAGGAGACTGCACCTCTTTAAGGCCATTGATTTGGTCTCTCTGTTCTTTAAACCA 651

Qy 166 GlyGluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluValLeuLys 185
 Db 652 GCGCAGAGGTTTAACGAAATCGTTGGTAGTCCGTACTACATGGCTCCGAGGTGCTAAAA 711

Qy 186 ArgAsnTyrGlyProGluValAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeu 205
 Db 712 CGGAATTTATGGTCCAGAAATGTGATATTGGAGTCAGGTGTAATTTCTTTTACATCTGCTA 771

Qy 206 CysGlyValProProPheTrpAlaGluThrGluGlnGlyValAlaLeuAlaIleLeuArg 225
 Db 772 TGTGGTCTCCGCTTTCTGGGCAGAACTGAACACAGAGGTTGCACACGCAATTTATTCCA 831

Qy 226 GlyValLeuAspPheLysArgAspProTyrSerGlnIleSerGluSerAlaLysSerLeu 245
 Db 832 TCTGTACTAGACTTCAGAGGGGCCATGCCCCAAGGTTTCTGAAAAACGCAAAAGACCTT 891

Qy 246 ValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGlnGlnValLeuAsp 265
 Db 892 ATCAGGAAATGCTTGATCTGACCAAAAGCGTCTTACAGCTCAACAGTCTCTAGAT 951

Qy 266 HisProTyrPileGlnAsnAlaLys 273

Db 952 CACCCGTGGTTACAGAAATGCAAG 975

RESULT 6

AAC47633

ID AAC47633 standard; DNA; 1836 BP.

XX AC AAC47633;

XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 54543.

XX

KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
XX promoter; termination sequence; ss.
XX Arabidopsis thaliana.
XX EP1033405-A2.
XX PD
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
XX 25-FEB-1999; 99US-0121825P.
XX 05-MAR-1999; 99US-0123180P.
XX 09-MAR-1999; 99US-0123548P.
XX 23-MAR-1999; 99US-0125788P.
XX 25-MAR-1999; 99US-0126264P.
XX 29-MAR-1999; 99US-0126785P.
XX 01-APR-1999; 99US-0127462P.
XX 06-APR-1999; 99US-0128234P.
XX 08-APR-1999; 99US-0128714P.
XX 16-APR-1999; 99US-0129845P.
XX 19-APR-1999; 99US-0130077P.
XX 21-APR-1999; 99US-0130449P.
XX 23-APR-1999; 99US-0130510P.
XX 23-APR-1999; 99US-0130891P.
XX 28-APR-1999; 99US-0131449P.
XX 30-APR-1999; 99US-0132048P.
XX 30-APR-1999; 99US-0132407P.
XX 04-MAY-1999; 99US-0132484P.
XX 05-MAY-1999; 99US-0132485P.
XX 06-MAY-1999; 99US-0132486P.
XX 06-MAY-1999; 99US-0132487P.
XX 07-MAY-1999; 99US-0132863P.
XX 11-MAY-1999; 99US-0134256P.
XX 14-MAY-1999; 99US-0134218P.
XX 14-MAY-1999; 99US-0134219P.
XX 14-MAY-1999; 99US-0134221P.
XX 14-MAY-1999; 99US-0134370P.
XX 18-MAY-1999; 99US-0134768P.
XX 19-MAY-1999; 99US-0134941P.
XX 20-MAY-1999; 99US-0135124P.
XX 21-MAY-1999; 99US-0135353P.
XX 24-MAY-1999; 99US-0135629P.
XX 25-MAY-1999; 99US-0136021P.
XX 27-MAY-1999; 99US-0136392P.
XX 28-MAY-1999; 99US-0136782P.
XX 01-JUN-1999; 99US-0137222P.
XX 03-JUN-1999; 99US-0137528P.
XX 04-JUN-1999; 99US-0137502P.
XX 07-JUN-1999; 99US-0137724P.
XX 08-JUN-1999; 99US-0138094P.
XX 10-JUN-1999; 99US-0138540P.
XX 10-JUN-1999; 99US-0138847P.
XX 14-JUN-1999; 99US-0139119P.
XX 16-JUN-1999; 99US-0139452P.
XX 17-JUN-1999; 99US-0139453P.
XX 18-JUN-1999; 99US-0139454P.
XX 18-JUN-1999; 99US-0139455P.
XX 18-JUN-1999; 99US-0139456P.
XX 18-JUN-1999; 99US-0139457P.
XX 18-JUN-1999; 99US-0139458P.
XX 18-JUN-1999; 99US-0139459P.
XX 18-JUN-1999; 99US-0139460P.
XX 18-JUN-1999; 99US-0139461P.
XX 18-JUN-1999; 99US-0139462P.
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XX 21-JUN-1999; 99US-0139817P.
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XX 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
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PR 19-JUL-1999; 99US-0144331P.
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PR 19-JUL-1999; 99US-0144333P.
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PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
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PR 27-AUG-1999; 99US-0151065P.
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PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.

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PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155488P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-015753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161408P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

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Alignment Scores:

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Pred. No.: 1.09e-124 Length: 1836
Score: 1161.00 Matches: 213
Percent Similarity: 88.43% Conservative: 24
Best Local Similarity: 79.48% Mismatches: 31
Query Match: 81.82% Indels: 0
DB: 3 Gaps: 0

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US-08-989-881-2 (1-274) x AAC47633 (1-1836)

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Qy 6 GlnlleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGlyGluPheGlyIleThr 25
Db 391 GAGATCGAGTCTAAATACACGTTGGGAGAGAGCTAGGTCGTGGAGAATTCGGTTACG 450
Qy 26 TyrLeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerIysArg 45
Db 451 TATCTATGACTGATGAAGAGACAGCAGCTTTTGGTTGTAATTCGATTTGAAGAAG 510
Qy 46 LysLeuArgThrAlaValAspValArgArgGluValThrIleMetSerThr 65
Db 511 AAGCTGAGGACAGCTGTTGATTAAGACATGTTAGGAGAGAGTTGAGATTATGAGGCAT 570
Qy 66 LeuProGluHisProAsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrVal 85
Db 571 ATGCTGAGCATCCTAATGTTGTTACTTTGAAGGAGACTTATGAGGATGAGCATGCTGTT 630

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Qy 86 HisLeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArgIleValAlaArgGly 105
Db 631 CATTTGGTTAAGGAGCTTTGAGAGGTGCTGAATTTGTTGATAGATTGTTGCTAGAGG 590
Qy 106 HisTyrThrGluArgAlaAlaThrValAlaArgThrIleAlaGluValValArgMet 125
Db 691 CATTATACTGAGAGAGCTGCTGCTGCTACTAAGACCATCATGAAAGTTGTTCCAGGTG 750
Qy 126 CysHisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsn 145
Db 751 TGTCAATAGCATGGGGTAATGCACAGGACCTGAAACCTGAGAACTTCTTGTTTGGAAC 810
Qy 146 LysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysPro 165
Db 811 AAGAGAGAGACTGCACCTCTTAAGCGGATTGATTTGGTCTCTCTGTTTCTTTAAACCA 870
Qy 166 GlyGluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluValLeuLys 185
Db 871 GCGGAGAGGTTTAAACGAAATCGTTGGTAGTCCGTACTACATGGCTCCGAGGTGCTAAA 930
Qy 186 ArgAsnTyrGlyProGluValAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeu 205
Db 931 CGGAATTATGCTCCAGAAAGTTGATATTGGAGTGCAGGTGTAATTTCTTACATACGCTA 990
Qy 206 CysGlyValProProPheTrpAlaGluThrGluGlnGlyValAlaLeuAlaIleLeuArg 225
Db 991 TGTGTTGTCCTCCCTTTCTGGCGAAGAACTGAAACAGAGATTGCACAGCAATTATTCCA 1050
Qy 226 GlyValLeuAspPheLysArgAspProTrpSerGlnIleSerGluSerAlaLysSerLeu 245
Db 1051 TCTGTACTAGACTTCAGAGGAGGCCCATGGCCCAAGGTTTCTGAAACGCAAAAGACCTT 1110
Qy 246 ValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGlnValLeuAsp 265
Db 1111 ATCAGGAAATGCTTGATCTCTGACCAAAAGCGCTGCTTACAGCTCAACAAAGTCTAGAT 1170
Qy 266 HisProTrpIleGlnAsnAlaLys 273
Db 1171 CACCCGTGTTACAGAAATGCANAG 1194

RESULT 7
AAF74280
ID AAF74280 standard; DNA; 1967 BP.
XX
AC AAF74280;
XX
DT 04-MAY-2001 (first entry)
XX
DE Strawberry calcium dependent protein kinase clone.
XX
KW Calcium dependent protein kinase; CDPK; herbicide resistance; paraquat;
KW diquat; crop production; ds.
XX
OS Fragaria x ananassa.
XX
PN WO200107592-A2.
XX
PD 01-FEB-2001.
XX
PF 26-JUL-2000; 2000WO-GB002876.
XX
PR 27-JUL-1999; 99GB-00017642.
XX
PA (ZENE ) ZENECA LTD.
XX
PI Holt CD, White AJ, Michael AJ, Osborn RW;
XX
DR WPI; 2001-169549/17.
XX
PT Producing herbicide resistance plants by inhibiting calcium dependent
PT protein kinase in plants or by providing an intracellular vacuolar
PT transporter capable of transporting agrochemical into plant vacuole.
XX

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PS Claim 18; Page 41; 50pp; English.
XX The present invention describes a method of producing plants which are
CC resistant to the herbicides paraquat and diquat, involving inhibiting in
CC the plants a calcium dependent protein kinase (CDPK) and selecting those
CC plants which are resistant to the agrochemical of interest. This is
CC useful in the production of crops with herbicide resistance
XX
SQ Sequence 1967 BP; 572 A; 334 C; 500 G; 561 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,69e-124 Length: 1967
Score: 1158.00 Matches: 215
Percent Similarity: 88.89% Conservative: 25
Best Local Similarity: 79.63% Mismatches: 30
Query Match: 81.61% Indels: 0
DB: 4 Gaps: 0

US-08-989-881-2 (1-274) x AAF74280 (1-1967)
Qy 5 ThrGlnIleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGlyGluPheGlyIle 24
Db 163 ACTGAATCAGCAGACACTTACGAGCTGGCGCGGAGCTCGCGCGGAGAGTTGCGGATT 222
Qy 25 ThrTyrLeuGlyThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerLys 44
Db 223 ACGTATCTGTGTACTGACAGGCCACCAACGAGAACTACGCTTGCAATCGATATCGAAG 282
Qy 45 ArgLysLeuArgThrAlaValAspValArgGluValThrIleMetSer 64
Db 283 CAGAACTGAGGACGGCTGTGGATATTGAAGTGTGAGGAGGAAGTTGAGATCATGAAG 342
Qy 65 ThrLeuProGluHisProAsnValValLysLysAlaThrTyrGluAspAsnGluThr 84
Db 343 CACTTGTCTAAGCATCCCAATATTGTGAGCTTGAAGATATTACGAGGATGATAATGCT 402
Qy 85 ValHisLeuValMetGluLeuGlyGlyGluLeuPheGlyArgIleValAlaArg 104
Db 403 GTCACTCTGTATGAGAGCTCTGTGAGGCGGTGAGCTTTTGTATCGATGCTGTCTAGG 462
Qy 105 GlyHisTyrThrGluArgAlaAlaThrValAlaArgThrIleAlaGluValValArg 124
Db 463 GGACATTACACTGAGCGTGTCTGTCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 522
Qy 125 MetCysHisValIleValMetHisArgAspLeuLysProGluAsnPheLeuPheAla 144
Db 523 ATGTGCCACAAAGCATGTGTGTGATGCACCGGATCTTAAACCTGAGAACTTTTGTTCGA 582
Qy 145 AsnLysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLys 164
Db 583 AACAGAAAGAAACAGCGCCCTTGAAGCAATTTGATTTGGTTGTCAGTGTCTTTAAG 642
Qy 165 ProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluValLeu 184
Db 643 CTTGGTGAAGATTCAGTGAATTTGTTGAAGTCCATACATACATGCTGCTGAGGTGCTA 702
Qy 185 LysArgAsnTyrGlyProGluValAspValTyrSerAlaGlyValIleLeuTyrIleLeu 204
Db 703 AGACGCAATTTATGCTCTGAAGTTGATGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 762
Qy 205 LeuCysGlyValProProPheTyrAlaGluThrGluGlnGlyValAlaLeuAlaIleLeu 224
Db 763 CTTTGTGTGTTCCGCTTTCTGGCAGAACTTGAACAGGAGGATGTCACCAAGCAATTTATA 822
Qy 225 ArgGlyValLeuAspPheLysArgAspProTyrSerGlnIleSerGluSerAlaLysSer 244
Db 823 CGGTCTGTGTAGATTTTAAAGAGGAGCCCTGCGCCCTAAAGGTTTCTGATATGCAAAAGAC 882
Qy 245 LeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGlnValLeu 264
Db 883 CTTGTGAAGAAGATGCTGTGATCTCTGACCCGAGCGGAGGCTTACAGCTCAGCAAGTTCTA 942
Qy 265 AspHisProTyrIleGlnAsnAlaLysLys 274

Db 943 GATCATACTTGGTTGCAAAATGCAAGAGA 972
RESULT 8
AAF74266
ID AAF74266 standard; DNA; 2087 BP.
XX
AC AAF74266;
XX
DT 04-MAY-2001 (first entry)
XX
DE Arabidopsis calcium dependent protein kinase clone #1.
XX
KW Calcium dependent protein kinase; CDPK; herbicide resistance; paraquat;
XX diquat; crop production; ds.
XX
OS Arabidopsis sp.
XX
PN WO200107592-A2.
XX
PD 01-FEB-2001.
XX
PF 26-JUL-2000; 2000WO-GB002876.
XX
PR 27-JUL-1999; 99GB-00017642.
XX
PA (ZENE ) ZENECA LTD.
XX
PI Holt CD, White AJ, Michael AJ, Osborn RW;
XX
WP1; 2001-168549/17.
XX
PT Producing herbicide resistance plants by inhibiting calcium dependent
PT protein kinase in plants or by providing an intracellular vacuolar
PT transporter capable of transporting agrochemical into plant vacuole.
XX
PS Claim 17; Page 33; 50pp; English.
XX
CC The present invention describes a method of producing plants which are
CC resistant to the herbicides paraquat and diquat, involving inhibiting in
CC the plants a calcium dependent protein kinase (CDPK) and selecting those
CC plants which are resistant to the agrochemical of interest. This is
CC useful in the production of crops with herbicide resistance
XX
SQ Sequence 2087 BP; 580 A; 391 C; 505 G; 611 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.4e-121 Length: 2087
Score: 1135.00 Matches: 209
Percent Similarity: 89.55% Conservative: 31
Best Local Similarity: 77.99% Mismatches: 28
Query Match: 79.99% Indels: 0
DB: 4 Gaps: 0

US-08-989-881-2 (1-274) x AAF74266 (1-2087)
Qy 7 IleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGlyGluPheGlyIleThrTyr 26
Db 360 ATCGAGGACCGTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTT 419
Qy 27 LeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerLysArgLys 46
Db 420 CTCTGTATCGAGGCTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 479
Qy 47 LeuArgThrAlaValAspValGluAspValAlaArgGluValThrIleMetSerThrLeu 66
Db 480 CTTAGAACTGCTGTGGATATTGAAGATGTTAAAGAGAGAGTAGCGGATTTATGAAGCATTTG 539
Qy 67 ProGluHisProAsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrValHis 86
Db 540 CTTAAGAGTTCGAGTATTGTTACTTTGAAAGAGAGCTTGTGAGGATGATTAATGCTGTGCAT 599
Qy 87 LeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArgIleValAlaArgGlyHis 106

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Db      1140 CCATGGATTGAGAACGCAAGAAA 1163
RESULT 10
IDA69918
ID      ADA69918 standard; DNA; 1770 BP.
XX
AC      ADA69918;
XX
DT      20-NOV-2003 (first entry)
DE      Rice gene, SEQ ID 3241.
XX
KW      Plant; bacterial infection; fungal infection; viral infection; rice;
KW      gene; ds.
XX
OS      Oryza sativa.
XX
PN      WQ2003000898-A1.
XX
PD      03-JAN-2003.
XX
PF      22-JUN-2001; 2001WO-IB001105.
XX
PR      22-JUN-2001; 2001WO-IB001105.
XX
PA      (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
PI      Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI      Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX
XX      WPI; 2003-175290/17.
XX
PT      Identifying at least one gene involved in plant resistance or response to
PT      pathogenic infection for conferring resistance or tolerance to a plant to
PT      bacterial, fungal or viral infection by determining or detecting plant
PT      gene expression.
XX
PS      Claim 6; SEQ ID NO 3241; 899pp; English.
XX
CC      The present invention relates to a method (M1) for identifying genes
CC      involved in plant resistance or response to pathogenic infection. M1
CC      comprises identifying a gene whose expression is significantly altered in
CC      the incompatible interaction of plant gene expression relative to
CC      expression of the gene in an uninfected plant, in a mutant plant that
CC      does not express a gene associated with response to pathogenic infection,
CC      or in a corresponding incompatible or compatible interaction. (M1) is
CC      useful for conferring resistance to resistance or tolerance to a plant to
CC      bacterial, fungal or viral infection. The present sequence was used to
CC      illustrate the invention.
XX
SQ      Sequence 1770 BP; 449 A; 394 C; 544 G; 383 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      2,48e-121      Length:      1770
Score:          1132.00      Matches:      211
Percent Similarity: 88.06%      Conservative: 25
Best Local Similarity: 78.73%      Mismatches: 32
Query Match:      79.77%      Indels:      0
DB:              8      Gaps:      0

US-08-989-881-2 (1-274) x ADA69918 (1-1770)

Qy      7 IleSerAspLysTyrIleLeuGluLeuGlyArgGluPheGlyIleThrTyr 26
Db      217 ATCGACGACAAAGTACGCGGAGCCGCGGAGCTCGGGGGGGGGAGTTCCGGGGTGACGTAC 276
Qy      27 LeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerLysArgLys 46
Db      277 CTGTGATGATCGGGACACCAAGAGCTCTCCCTGCAAGTCCATCTCCAAGCGGAAG 336
Qy      47 LeuArgThrAlaValAspValGluAspValArgGluValThrIleMetSerThrLeu 66
Db      337 CTGAGGACGCGGTTCGACGTTGGAGGAGCTCGCGCGGGAGGTCCGCTCATGTCGCCACCTC 396

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Qy      67 ProGluHisProAsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrValHis 86
Db      397 CCCAAGAGCGCCAGCATCGTCTCGCTCGGAGGCGTGCAGGACGACGAGGCGCGTGCAC 456
Qy      87 LeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArgIleValAlaAsgGlyHis 106
Db      457 CTCGTGATGAGCTCTCGAAGCGGGAGCTCTTCGACCGCATCGTGGAGGTCTGCGCGGGGCCAC 516
Qy      107 TyrThrGluArgAlaAlaThrValAlaAArgThrIleAlaGluValValArgMetCys 126
Db      517 TACACGAGCGCGCGCCCAATGTCAACCGCACCATCGTGGAGGTCTGCGCGGGGCCAC 576
Qy      127 HisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsnLys 146
Db      577 CACCGCCACGGCGTTATCCACCGGACCTCAAGCCCGGAGAACTTCTCTTCGCGCAACAG 636
Qy      147 LysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysProGly 166
Db      637 AAGGAACTCGCCGCTCAAGGCCATCGATTTCCGGCTCTCCATCTTCTTCAAGCCCGGT 696
Qy      167 GluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluValLeuLysArg 186
Db      697 GAGAACTTTCTGAAATTTGGGAAGCCCATATTACATGGCTCCAGAGGTATTGAAGAGA 756
Qy      187 AsnTyrGlyProGluValAspValTrpSerAlaGlyValIleLeuTyrIleLeuLysCys 206
Db      757 AACTATGGTCCGAAATAGATATTGGAGTGCAGGAGTTATCTTGTATATTTTGTATGT 816
Qy      207 GlyValProPheThrAlaGluThrGluGlnGlyValAlaLeuAlaIleLeuArgGly 226
Db      817 GGAGTTCTCCATTTTGGGCTGAGACTGAGCAAGGGGTGGCAAGCCATCTTCTGTGGA 876
Qy      227 ValLeuAspPheLysArgAspProTrpSerGlnIleSerGluSerAlaLysSerLeuVal 246
Db      877 AATATCGATTTCAACGCGAACCCCTGGCCAAATGTTTCAGAAAATGCTAAAGATTGGTT 936
Qy      247 LysGluMetLeuGluProAspSerThrLysArgLeuThrAlaGlnGlnValLeuAspHis 266
Db      937 CGACGCAATGTTGGAGCTCATCCAAACTCAGGTTAACTGCAAGCAAGTCTTGAACAT 996
Qy      267 ProTrpIleGluAsnAlaLysLys 274
Db      997 CCATGGCTTCAAAATGCTAAGAAA 1020
RESULT 11
ADJ39574
ID      ADJ39574 standard; cDNA; 1770 BP.
XX
AC      ADJ39574;
XX
DT      06-MAY-2004 (first entry)
XX
DE      Plant cDNA #574.
XX
KW      Plant; gene; ss; transcription; plant genome augmentation; cereal;
KW      soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
KW      maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
KW      stress tolerance; salt tolerance; cold tolerance; drought tolerance;
KW      plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
KW      antifungal.
XX
OS      Eukaryota.
XX
PN      US2004016025-A1.
XX
PD      22-JAN-2004.
XX
PF      26-SEP-2002; 2002US-00260238.
XX
PR      26-SEP-2001; 2001US-0325277P.
PR      26-SEP-2001; 2001US-0325448P.
PR      04-APR-2002; 2002US-0370620P.

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XX (BUDW/) BUDWORTH P.
PA (MOUW/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVANT N.
PA (RICK/) RIQUE D.
PA (ZHUT/) ZHU T.
XX
PI Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J;
PI Goff SA, Katagiri F, Provant N, Ricke D, Zhu T;
XX
DR WPI; 2004-190374/18.
XX
XX New rice promoter, useful for manipulating crop plants to alter or
PT improve phenotypic characteristics, e.g. produce large quantities of oil
PT or proteins, resistance to insecticides, virus or fungi, stress tolerance
PT or high nutritional value.
XX
XX Claim 70; SEQ ID NO 574; 230bp; English.
XX
XX The invention relates to plant nucleotide sequences that direct seed-,
CC leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential
CC or constitutive transcription of an operatively linked nucleic acid
CC segment. The invention also relates to a method for augmenting a plant
CC genome and a method of identifying a gene, where its expression is
CC altered in the seed, leaf, stem, panicle, pollen, root or is constitutive
CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
CC sorghum, rice or wheat. The polynucleotides and the polypeptides they
CC encode are useful for manipulating crop plants to alter or improve
CC phenotypic characteristics, to produce large quantities of oil or
CC proteins, to incur resistance to insecticides, viruses or fungi, and to
CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
CC have a high nutritional value with reduced apical dominance or dwarfism,
CC early flowering or altered metabolic pathways. This sequence represents a
CC plant nucleic acid of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification but was obtained in
CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX SQ Sequence 1770 BP; 449 A; 394 C; 544 G; 383 T; 0 U; 0 Other;

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Alignment Scores:

Pred. No.:	2.48e-121	Length:	1770
Score:	1132.00	Matches:	211
Percent Similarity:	88.06%	Conservative:	25
Best Local Similarity:	78.73%	Mismatches:	32
Query Match:	79.77%	Indels:	0
DB:	12	Gaps:	0

US-08-989-881-2 (1-274) x ADJ39574 (1-1770)

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Oy 7 IleSerAspLysThrIleLeuGlyArgGluLeuGlyArgGlyGluPheGlyIleThrTyr 26
Db 217 ATCCACGACCAAGTACCGCTGGACCGGAGCTCGGGCGGGGGAGTTCCGGGTGACGTAC 276
Oy 27 LeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerLysArgLys 46
Db 277 CTGTGCATGATCGGGACACCAAGAGAGCTGCTCCCTGCAAGTCCATCTCCACGGGAG 336
Oy 47 LeuArgThrAlaValAspValGluAspValArgGluValThrIleMetSerThrLeu 66
Db 337 CTGAGGACGGCGGTGCGACGTGGAGGAGCTGCGCGGGAGGTGCGCATCATCGCCACCTC 396
Oy 67 ProGluHisProAsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrValHis 86
Db 397 CCCAAGAGCGCCAGCATCGTCTCGTCGGGAGCGGTGCGAGGACGAGGGCGCGTGCAC 456
Oy 87 LeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArgIleValAlaArgGlyHis 106

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Db 457 CTCGTCATGGAGCTCTGGAGAGCGGGAGGCTCTTCGACCGCATCGTCGCGGGGCCAC 516
Oy 107 TyrThrGluArgAlaAlaIaIaThrValAlaAargThrIleAlaGluValValargMetCys 126
Db 517 TACACGGAGCGCGCGCGCAATGTCCACCGCACCATCGTGGAGGTGCTCCAGCTGCTGC 576
Oy 127 HisValAsnGlyValMetHisAargAspLeuLysProGluAsnPheLeuPheAlaAenLys 146
Db 577 CACCGCCACGCGGTATCCACCGGAGCTCAAGCCCGGAGAACTTCCTCTTCGCCAACAG 636
Oy 147 LysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysProGly 166
Db 637 AAGGAGAACTCGCGCTCAAGGCCATCGATTTTCGCGCTCTCCATCTTCTCAAGCCCGT 696
Oy 167 GluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluValLeuLysArg 186
Db 697 GAGAAGTTTCTGAAATTTGGGAAGCCCATATTACATGGCTCCAGAGGTATTGAAGAGA 756
Oy 187 AsnTyrGlyProGluValAspValTyrSerAlaGlyValIleLeuTyrIleLeuLys 206
Db 757 AACTATGTCGCGAAATAGATATTGGAGTGCAGAGTATCTTGTATATTATTGTATGT 816
Oy 207 GlyValProPheTrpAlaGluThrGluGlnGlyValAlaLeuAlaIleLeuArgGly 226
Db 817 GGAGTCTCTCATTTTGGGCTGAGACTGACGAGGGTGGCACAGCCATTTCTTCGTGA 876
Oy 227 ValLeuAspPheLysArgAspProTyrSerGlnIleSerGluSerAlaLysSerLeuVal 246
Db 877 AATATCATGATTTCAACCGCAACCTCGGCAAAATGTTTCAAGAAATGCTAAAGATTGGTT 936
Oy 247 LysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGlnGlnValLeuAspHis 266
Db 937 CGAGCATGTGGAGCTGATCCAAACTCAGGTAACTGCAAAAGCAAGTTCTTGAACAT 996
Oy 267 ProTrpIleGlnAsnAlaLysLys 274
Db 997 CCATGGCTTCAAAATGCTAAGAA 1020

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RESULT 12
ABZ14499
ID ABZ14499 standard; DNA; 1602 BP.

AC ABZ14499;
XX 21-JAN-2003 (first entry)
DT
XX Arabidopsis thaliana stress regulated gene SEQ ID NO 2304.
DE Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
KW Arabidopsis thaliana.
XX Arabidopsis thaliana.
OS
XX WO200216655-A2.
PN
XX 28-FEB-2002.
PD
XX 24-AUG-2001; 2001WO-US026685.
PF
XX 24-AUG-2000; 2000US-0227866P.
PR 26-JAN-2001; 2001US-0264647P.
PR 22-JUN-2001; 2001US-0300111P.
XX (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
PI Harper JF, Kreps J, Wang X, Zhu T;
XX WPI; 2002-304127/34.
DR
XX Identifying a stress condition to which a plant cell has been exposed and
PT producing plants with increased tolerance to these abiotic stresses.

PS Claim 144; SEQ ID NO 2304; 577pp + Sequence Listing; English.

XX The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present invention is that of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office

XX SQ Sequence 1602 BP; 483 A; 265 C; 444 G; 410 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8,23e-121 Length: 1602
Score: 1127.00 Matches: 211
Percent Similarity: 88.06% Conservative: 25
Best Local Similarity: 78.73% Mismatches: 32
Query Match: 79.42% Indels: 0
DB: 6 Gaps: 0

US-08-989-881-2 (1-274) x AB214499 (1-1602)

QY 7 IleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGluPheGlyIleThrTyr 26
DB 157 ATATCTTATGATGATCTGGCGGTGAGTTGGTCGCGAGAGTTGGTATTACTTAC 216
QY 27 LeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerLysArgLys 46
DB 217 TTGTGCACCTGATATCAAAACGGCGAGAGATATGCGTGAAGTCTATATCAAGAAGAAG 276
QY 47 LeuArgThrAlaValAspValGluAspValArgValArgValThrIleMetSerThrLeu 66
DB 277 CTTAGAACAGCTGTGGATATAGAGGATGTAGAGGGAAGTTGAGATATGAACATATG 336
QY 67 ProGluHisProAsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrValHis 86
DB 337 CCTAGACACCAATATCGTGCCTGAAGGATGCCTTTGAGGATGATGATGAGTGCAT 396
QY 87 LeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyValAlaArgGlyHis 106
DB 397 ATAGTTATGAGTTGTGTAAGGAGGTGAGCTGTTGATCGGATGTGCTAGAGTGCAT 456
QY 107 TyrThrGluArgAlaAlaAlaThrValAlaArgThrIleAlaGluValValArgMetCys 126
DB 457 TATACTGAGCGAGCTGCTGCTGAGTATGAAGACTATTCTTCAAGTTGTTCAAGATGC 516
QY 127 HisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsnLys 146
DB 517 CATAAGCATGGAGTGTATCGGATCGGGATCTAAAGCCTGAGAAGTTCTCTTTGCAAAATAA 576
QY 147 LysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysProGly 166
DB 577 AAAGACATCAGCCCTTAAAGCCATAGATTTTGGATTATCAGTCTCTTCAAGCCTGCT 636
QY 167 GluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluValLeuLysArg 186
DB 637 GAGGGATTCAACAGAGATTGTTGAAGTCTTATTACATGCGCAGAGGTTACTTAGGCGA 696
QY 187 AsnTyrGlyProGluValAspValTrpSerAlaGlyValIleLeuTyrIleLeuLysCys 206
DB 697 AATTACGGACCTGAGTGTATATCTGGAGTGTGAGGATATCTCTTATATCTTCTGCTGT 756
QY 207 GlyValProPheThrPalaGluThrGluGlnGlyValAlaLeuAlaIleLeuArgGly 226
DB 757 GGTGTCCACCATTTTGGGCGAGACTGACCAAGGGGTGCTCAGCGCATCATTAGGTCA 816
QY 227 ValLeuAspPheLysArgAspProTrpSerGlnIleSerGluSerAlaLysSerLeuVal 246

DB 817 GTTATCGACTTTAAGAGGGATCCATGGCCGAGAGTTTCTGAGACTGCCAAAGACCTTGTG 876
QY 247 LysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGlnGlnValLeuAspHis 266
DB 877 AGGAAGATCTCTGAACCTTGACCCCAAAACCGCTTTCTGCTGCACAAGTACTCGAACAT 936
QY 267 ProTrpIleGlnAsnAlaLysLys 274
DB 937 TCTTGATACAAATGCGAAG 960

RESULT 13

AAF74263

ID AAF74263 standard; DNA; 1726 BP.

XX AAF74263;

XX 04-MAY-2001 (first entry)

XX Arabidopsis calcium dependent protein kinase clone 15-1.

XX Calcium dependent protein kinase; CDPK; herbicide resistance; paraquat;

XX diquat; crop production; ds.

XX Arabidopsis sp.

XX WO200107592-A2.

XX 01-FEB-2001.

XX 26-JUL-2000; 2000WO-GB002876.

XX 27-JUL-1999; 99GB-00017642.

XX (ZENE) ZENECA LTD.

XX Holt CD, White AJ, Michael AJ, Osborn RW;

XX WPI; 2001-168549/17.

XX Producing herbicide resistance plants by inhibiting calcium dependent protein kinase in plants or by providing an intracellular vacuolar transporter capable of transporting agrochemical into plant vacuole.

XX Claim 17; Page 32; 50pp; English.

XX The present invention describes a method of producing plants which are resistant to the herbicides paraquat and diquat, involving inhibiting in the plants a calcium dependent protein kinase (CDPK) and selecting those plants which are resistant to the agrochemical of interest. This is useful in the production of crops with herbicide resistance

XX SQ Sequence 1726 BP; 518 A; 279 C; 449 G; 480 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9,14e-121 Length: 1726
Score: 1127.00 Matches: 211
Percent Similarity: 88.06% Conservative: 25
Best Local Similarity: 78.73% Mismatches: 32
Query Match: 79.42% Indels: 0
DB: 4 Gaps: 0

US-08-989-881-2 (1-274) x AAF74263 (1-1726)

QY 7 IleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGluPheGlyIleThrTyr 26
DB 51 ATATCTTATGATGATCTGGCGGTGAGTTGGTCGCGAGAGTTGGTATTACTTAC 110
QY 27 LeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerLysArgLys 46
DB 111 TTGTGCACCTGATATCAAAACGGCGAGAGATATGCGTGAAGTCTATATCAAGAAGAAG 170
QY 47 LeuArgThrAlaValAspValGluAspValArgGluValThrIleMetSerThrLeu 66

Db 171 CTTAGAACAGCTGTGGATATAGAGGATGTTAGGAGGAAGTTGAGATAATCAACATATG 230
 Qy 67 ProGluHisProAsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrValHis 86
 Db 231 CCTAGACACCAATATCGTTCGCTGAAGATGCTTTGAGGATGATGATGCGATGCGAT 290
 Qy 87 LeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArgGlyLeuValAlaArgGlyHis 106
 Db 291 ATAGTTATGGATTGTGTGAAGGAGTGAGTGTGTTGATCGATGTTGCTAGAGTTCAT 350
 Qy 107 TyrThrGluArgAlaAlaAlaThrValAlaAlaArgThrLeuAlaGluValValArgMetCys 126
 Db 351 TATATCTGAGCGAGCTGCTGCTGCACTGATGAAGACTATCTTGAAGTTGTTTCAGATATG 410
 Qy 127 HisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsnLys 146
 Db 411 CATAAGCATGAGTGATGATCGGAGTCTAAAGCTGAGAACTTTCTCTTTGCAATAAA 470
 Qy 147 LysGluAsnSerAlaLeuLysAlaAlaLeuAspPheGlyLeuSerValLeuPheLysProGly 166
 Db 471 AAAGAGACATCAGCCCTTAAAGCCATAGATTTTGATATCAGTCTTCTTCAAGCCTGGT 530
 Qy 167 GluArgPheThrGluLeuValGlySerProTyrTyrMetAlaProGluValLeuLysArg 186
 Db 531 GAGGATTCACAGAGATTGTTGGAAGTCTTATTACATGGCCACAGAGGTTACTTAGCGCA 590
 Qy 187 AsnTyrGlyProGluValAspValTrpSerLaglyValLeuLysLeuLysCys 206
 Db 591 AATTACGGACCTGAGTTGATATCTGGAGTCTGGAGTTATCTTTTATATCTCTCTGT 650
 Qy 207 GlyValProPheTrpAlaGluThrGluGlnGlyValAlaLeuAlaLeuArgGly 226
 Db 651 GGTGTCACCATTTTGGCCGACACTGAGCAAGGGTGGCTCAGGCGATCATTAGGTCA 710
 Qy 227 ValLeuAspPheLysArgAspProTrpSerGlnLysSerGluSerAlaLysSerLeuVal 246
 Db 711 GTTATCGACTTAAAGAGGATCCATGCGGAGAGTTTCTGAGACTGCCAAGACCTTGTG 770
 Qy 247 LysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGlnGlnValLeuAspHis 265
 Db 771 AGGAAGATGCTCGAACTGACCCCAAAACCGGCTTTCTGCTGCACAACTACTCGAACAT 830
 Qy 267 ProTrpIleGlnAsnAlaLysLys 274
 Db 831 TCTTGGATACAAATGCGAAGAG 854
 RESULT 14
 ID ADF38032
 AC ADF38032 standard; cDNA; 1868 BP.
 XX
 AC ADF38032;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Synchronised tobacco BY2 cDNA sequence SEQ ID NO:91.
 XX
 KW identification; validation; plant; agrochemical; gene; ss.
 XX
 OS Nicotiana tabacum.
 XX
 PN WO2003085115-A2.
 XX
 PD 16-OCT-2003.
 XX
 PF 08-APR-2003; 2003WO-EP003703.
 XX
 PR 10-APR-2002; 2002EP-00447062.
 PR 15-JUL-2002; 2002US-0396124P.
 XX
 XX (CROP-) CROPPDESIGN NV.
 PA
 XX Inze D, Broekaert W;
 PI
 XX

WPI; 2003-804308/75.
 Identifying and validating plant genes or proteins as targets for agrochemicals, useful for producing agrochemical-resistant plants, comprises determining and down regulating the gene or protein expression profiles of a plant.
 Claim 12; SEQ ID NO 91; 183pp; English.
 The present invention describes a method for identifying and validating plant genes/proteins as targets for agrochemicals comprising determining the gene or protein expression profiles of a plant and downregulating the expression of the gene or protein in the plant or plant cell. Also described: (1) methods for screening candidate agrochemical compounds, comprising the use of the above method or the use of any of the 785 fully defined nucleotide sequences (ADF37942 to ADF38726) or protein sequences, or their homologues, functional fragments or derivatives; (2) a method for producing an agrochemical resistant plant, comprising the use of the above-mentioned nucleotide or protein sequences; (3) an isolated nucleic acid that is identified by any of the above methods or that comprises at least a part of a nucleic acid sequence chosen from any of the 785 nucleotide sequences given in the specification; (4) a plant tolerant to an agrochemical, in which the expression level of one or more of the nucleic acid sequences given in the specification is modulated; and (5) a harvestable part of the plant described above. The method is useful in: identifying and validating plant targets for agrochemicals or in producing an agrochemical resistant plant. The nucleic acid or protein can be used as a target for an agrochemical compound, particularly herbicide. The present sequence represents a synchronised tobacco BY2 cDNA nucleotide sequence which is used in the exemplification of the present invention.
 SEQ Sequence 1868 BP; 553 A; 328 C; 470 G; 517 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2,28e-120 Length: 1868
 Score: 1124.00 Matches: 209
 Percent Similarity: 87.41% Conservative: 27
 Best Local Similarity: 77.41% Mismatches: 34
 Query Match: 19.21% Indels: 0
 DB: 10 Gaps: 0
 US-08-989-881-2 (1-274) x ADF38032 (1-1868)
 Qy 5 ThrGlnIleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGlyGluPheGlyIle 24
 Db 235 TCGAACGTTGAAGAGAGTATTATTAGTTGATAGAGAACTAGCGAGGGCGGAATTCGGAAT 294
 Qy 25 ThrTyrLeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerLys 44
 Db 295 ACATACCTTTGTATAGATCGTAACAGTAAAGAGCTTTAGCTTCCAAGTCAATTTCAAAA 354
 Qy 45 ArgLysLeuArgThrAlaValAspValGluAspValArgGluValThrIleMetSer 64
 Db 355 CGGAAGCTACGAACAGCTGTAGATGTGGAAGAGCTGAGGAGAGAGTAGCCATAATGAAG 414
 Qy 65 ThrLeuProGluHisProAsnValValLysLeuLysAlaThrTyrGluAspAsnGluThr 84
 Db 415 CATTTCCCGGTGAATTCGAAGTATTGTGAGCTTTAGAGAAAGCTTGTGAGGATGAAATGCG 474
 Qy 85 ValHisLeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArgGlyLeuValAlaArg 104
 Db 475 GTGCATTTGGTTATGGAATTTGCGAAGGTGGGGAATTTGTCATAGATTGTGGCCGGA 534
 Qy 105 GlyHisTyrThrGluArgAlaAlaAlaThrValAlaAlaArgThrIleAlaGluValValArg 124
 Db 535 GGACATTATATCTGAACGAGCTGCTGCTGTGTACACGGACGATTTGGAGGTTGTGATG 594
 Qy 125 MetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAla 144
 Db 595 CTTTGTGTAAGCATGTTGTTGATTCATCGAGATTTGAAACCTGAGAACTTTTGTATGCT 654
 Qy 145 AsnLysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLys 164

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Db 655 AATAAGAGAAATTCGCCTCTTAAAGCTATTGATTTGGCTGTGCAATTTCTTCAAG 714
Qy 165 ProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluValLeu 184
Db 715 CCAGGTGAGAGGTTCTCTGAATAGTCGAAGTCCCTATTATATGCTCTCGAGGTGCTC 774
Qy 185 LysArgAsnTyrGlyProGluValAspValTrpSerAlaGlyValIleLeuTyrIleLeu 204
Db 775 AAACGAAATCATGGACCAAGAAATAGATATATGAGTGCAGGAGTCAATTTATATATTTG 834
Qy 205 LeuCybGlyValProPheTyrAlaGluThrGluGlnGlyValAlaLeuAlaIleLeu 224
Db 835 TTATGTGGGGTTCCTCTTTTGGCGGAATCTGAACAAGGTGTGCTCAGGCCATCTTA 894
Qy 225 ArgGlyValLeuAspPheLysArgAspProTyrTrpSerGlnIleSerGluSerAlaLysSer 244
Db 895 CGTGGGTGATAGATTCAACCGGAACCTGCGCAAGTATTTTCAGAGAGTGCTAAAAAT 954
Qy 245 LeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGlnValLeu 264
Db 955 CTTGTACGGCAATGCTGAACACAGATCCAAAGCTTCGACTGACTGACAAACAAGTACTT 1014
Qy 265 AspHisProTyrIleGlnAsnAlaLysLys 274
Db 1015 GAACACTCTTGGCTCAAAATGCTAAGAG 1044

RESULT 15
ADA70638
ID ADA70638 standard; DNA; 1515 BP.
XX AC ADA70638;
XX 20-NOV-2003 (first entry)
DE Rice gene, SEQ ID 3961.
XX Plant; bacterial infection; fungal infection; viral infection; rice;
KW gene; ds.
XX Oryza sativa.
XX WO200300898-A1.
XX 03-JAN-2003.
XX 22-JUN-2001; 2001WO-IB001105.
XX 22-JUN-2001; 2001WO-IB001105.
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
XX Katagiri F, Qian S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX WPI; 2003-175290/17.
XX Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting a plant
PT gene expression.
XX Claim 6; SEQ ID NO 3961; 899pp; English.
XX The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
```

CC illustrate the invention.

XX SQ Sequence 1515 BP; 395 A; 344 C; 467 G; 309 T; 0 U; 0 Other;

Alignment Scores:

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Pred. No.: 1.9e-119 Length: 1515
Score: 1115.00 Matches: 207
Percent Similarity: 88.30% Conservative: 27
Best Local Similarity: 78.11% Mismatches: 31
Query Match: 78.58% Indels: 0
DB: 8 Gaps: 0
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US-08-989-881-2 (1-274) x ADA70638 (1-1515)

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Qy 10 LysTyrIleLeuGlyArgGluLeuGlyArgGlyGluPheGlyIleThrTyrLeuCybThr 29
Db 187 CGGTACAGAGTCGGCGGAGCTGGGCGCGGAGTTCGGGATCACGTACCTGTGCACG 246
Qy 30 AspArgGluThrArgGluAlaLeuAlaCybLysSerIleSerLysArgLysLeuArgThr 49
Db 247 GAGCGGAGACGGGACAGGTACCGTGCAGTGCATATCGAAGGGAAGCTGCGGACG 306
Qy 50 AlaValAspValGluAspValArgArgGluValThrIleMetSerThrLeuProGluHis 69
Db 307 CGGTGGAGCTGGAGACGTGCGCGGAGGTGGAGATCATGCCACATGCCGTGCGCAT 366
Qy 70 ProAsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrValHisLeuValMet 89
Db 367 CCGAATCATGTCAGGCTCGCGCCCTACGAGGACGAGCAACGTCACCTCGTCATG 426
Qy 90 GluLeuCybGluGlyGluLeuPheGlyArgIleValAlaArgGlyHisTyrThrGlu 109
Db 427 GAGCTCTGGAGGCGGCGAGCTCTTCGACAGAGTCTGCGCGGGGCCACTACACGAG 486
Qy 110 ArgAlaAlaAlaThrValAlaArgThrIleAlaGluValValArgMetCysHisValAsn 129
Db 487 CGCGCGCGCGCGCTCACGCCACCATCGTCGAGGTGGTTCAGATGTGCCACAGCAT 546
Qy 130 GlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsnLysLysGluAsn 149
Db 547 GGTGTATGTCACCGGACCTTAAACCAAGAAATCTTCCTATATGCTAACCAAGAGGATAGT 606
Qy 150 SerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysProGlyGluArgPhe 169
Db 607 TCTCTCTGAAGCAATTGATTTTGGGCTATCTGTGTTCTTCAGGCTCGTGAGCGGTTT 666
Qy 170 ThrGluIleValGlySerProTyrTyrMetAlaProGluValLeuLysArgAsnTyrGly 189
Db 667 ACTGAAATTTGAGGAGTCCATATTTACATGGCTCCAGAGGTTTAAAGCGACACTATGTC 726
Qy 190 ProGluValAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeuCybGlyValPro 209
Db 727 CTTGAAGTTGATGCTGGAGTGCAGAGTGATCTTACATACTCTTTTCGGGTGTACCA 786
Qy 210 ProPheTyrAlaGluThrGluGlnGlyValAlaLeuAlaIleLeuArgGlyValLeuAsp 229
Db 787 CCATTTTGGCAGAAACCGAGGAGTAGCGAGGCAATTTATAGCTCTGTGTGTAGAT 846
Qy 230 PheLysArgAspProTyrTrpSerGlnIleSerGluSerAlaLysSerLeuValLysGlnMet 249
Db 847 TTCAAAAGAGAACCATGGCCAGGGTATCTGAGCCAGCTAAAGATCTTCTGTAAGCGGATG 906
Qy 250 LeuGluProAspSerThrLysArgLeuThrAlaGlnValLeuAlaAspHisProTyrPile 269
Db 907 TTGGACCAATTTCCCATGACAAGGCTTACTGCAGAACAAAGTACTTGAACATCATGTTA 966
Qy 270 GlnAsnAlaLysLys 274
Db 967 CATGATTTCTAAAAAG 981
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	792.5	55.8	4162	2	US-08-459-448A-26
2	792.5	55.8	4162	3	US-08-459-595A-26
3	792.5	55.8	4162	3	US-08-459-504B-26
4	792.5	55.8	4162	3	US-08-459-444-26
5	792.5	55.8	4162	3	US-09-547-422-26
6	792.5	55.8	4162	4	US-09-988-462-26
7	792.5	55.8	4165	1	US-07-951-715A-26
8	699	49.3	1349	1	US-07-951-715A-20
9	699	49.3	1349	2	US-08-459-448A-20
10	699	49.3	1349	3	US-08-459-595A-20
11	699	49.3	1349	3	US-08-459-504B-20
12	699	49.3	1349	3	US-08-459-444-20

13	699	49.3	1349	3	US-09-547-422-20	Sequence 0, Appli
14	699	49.3	1349	4	US-09-988-462-20	Sequence 20, Appl
15	697	49.1	2374	3	US-09-347-801-3	Sequence 3, Appli
16	697	49.1	2374	4	US-09-854-731-3	Sequence 3, Appli
17	524.5	37.0	1400	1	US-08-464-164-1	Sequence 1, Appli
18	524.5	37.0	1400	1	US-08-338-057-1	Sequence 1, Appli
19	524.5	37.0	1400	2	US-08-668-416-1	Sequence 1, Appli
20	515	36.3	2061	3	US-09-800-960-1	Sequence 1, Appli
21	515	36.3	2061	4	US-10-096-960-1	Sequence 1, Appli
22	514	36.2	1442	4	US-09-949-016-1590	Sequence 1590, Ap
23	514	36.2	1442	4	US-09-949-016-1591	Sequence 1591, Ap
24	514	36.2	1480	4	US-09-016-434-1454	Sequence 1454, Ap
25	509	35.9	2447	4	US-09-960-643-1	Sequence 1, Appli
26	508	35.8	2218	4	US-09-820-790B-1	Sequence 1, Appli
27	506	35.7	1458	4	US-09-230-896C-5	Sequence 5, Appli
28	504.5	35.6	1776	3	US-08-655-352-10	Sequence 10, Appl
29	504.5	35.6	1776	3	US-09-258-016-10	Sequence 10, Appl
30	504.5	35.6	1776	3	US-09-257-825B-10	Sequence 10, Appl
31	502.5	35.4	2454	4	US-09-992-481-3	Sequence 3, Appli
32	502.5	35.4	2454	4	US-10-434-034-3	Sequence 3, Appli
33	502.5	35.4	2824	4	US-09-992-481-5	Sequence 5, Appli
34	502.5	35.4	2824	4	US-10-434-034-5	Sequence 5, Appli
35	498	35.1	1074	4	US-09-733-388-3	Sequence 3, Appli
36	498	35.1	1074	4	US-10-446-175-3	Sequence 3, Appli
37	498	35.1	1158	4	US-09-733-388-1	Sequence 1, Appli
38	498	35.1	1158	4	US-10-416-175-1	Sequence 1, Appli
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41	498	35.1	1694	4	US-09-579-664B-3	Sequence 3, Appli
42	498	35.1	1694	4	US-10-355-975A-3	Sequence 3, Appli
43	498	35.1	1733	4	US-09-620-312D-526	Sequence 526, App
44	495.5	34.9	2165	4	US-09-620-312D-809	Sequence 809, App
45	492.5	34.7	1584	4	US-09-799-451-205	Sequence 205, App

ALIGNMENTS

RESULT 1
US-08-459-448A-26
; Sequence 26, Application US/08459448A
; Patent No. 5859336
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Croesland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5859336artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; STREET: Rd., POB 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

QY 111 AlaAlaAlaThrValAlaAaGrThrIleAlaGluValValArgMetCysHisValAsnGly 130
Db 2057 GGGCGCGCGAGTGTGCGCGCATGTGCAGATGTGCACACCTCCACCTCCATGGG 2116
QY 131 ValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsnLysLysGluAsnSer 150
Db 2117 GTGATGCCCGGACATCAAGCCGAGAACTTCTGTCTCAGCAAGGAGGAGCGG 2176
QY 151 AlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysProGluA-rgPheThr 170
Db 2177 CCGTCAAGGCCACCGACTTCGGCTCTCGCTCTTCTTCAAGGAGGCGGCTCAGG 2236
QY 171 GluIleValGlySerProTyrTyrMetAlaProGluValLeuLysArgAsnTyrGlyPro 190
Db 2237 GACATCTGCGCAGCGCTACTACTCGCCCGAGGTCTCAAGAGGAAGTACGCGCCG 2296
QY 191 GluValAspValTrpSerAlaGlyValIleLeuTyrIleLeuLysGlyValProPro 210
Db 2297 GAGCGCGACATCTGGAGCGTGGCGTCTATCTCTACATCTTCTCGCGCGGTGCTCC 2356
QY 211 PheTrpAla----- 213
Db 2357 TTCTGGGC-AGTTCGGATCGTCTCGTGTCTCTAGACGATATACAGAACCCGACGATG 2415
QY 214 -----GluThrGluGlnGlyValAlaLeuAla 222
Db 2416 GATTGCTTCTAGCCCTGTTTGTGATCACCAGAGAACGAGCATCTTCCACGCC 2475
QY 223 IleLeuArgGlyValLeuAspPheLysArgAspProTrpSerGlnIleSerGluSerAla 242
Db 2476 ATCTGCGAGGCGAGCTTGACCTCTCCAGCGAGCATGGCCACACATCTCGCGGGAGCC 2535
QY 243 LysSerLeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGlnGln 262
Db 2536 AAGGATCTCGTCAAGAGATGCTCAACATCAACCCCAAGGAGCGGCTCACGGGGTTCCAG 2595
QY 263 ValLeu 264
Db 2596 GTCTC 2601

RESULT 3

US-08-459-504B-26
Sequence 26, Application US/08459504B
Patent No. 6075185

GENERAL INFORMATION:

APPLICANT: Kozziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6075185artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,504B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 4162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1418..1427
OTHER INFORMATION: /note= "start of mRNA"
FEATURE:
NAME/KEY: exon
LOCATION: 1481..2366
FEATURE:
NAME/KEY: intron
LOCATION: 2367..2451
FEATURE:
NAME/KEY: exon
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LOCATION: 2603..2690
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LOCATION: 3178..3304
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LOCATION: 3305..3398
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NAME/KEY: intron
LOCATION: 3499..3713
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NAME/KEY: exon
LOCATION: 3714..3811

US-08-459-504B-26

Alignment Scores:

Pred. No.: 9.45e-92 Length: 4162
Score: 792.50 Matches: 159
Percent Similarity: 66.67% Conservative: 29
Best Local Similarity: 56.38% Mismatches: 66
Query Match: 55.85% Indels: 29
DB: 3 Gaps: 1

US-08-989-881-2 (1-274) x US-08-459-504B-26 (1-4162)

Qy 11 TyrIleuGlyArgGluGlyArgGlyGluPheGlyIleThrTyrLeuCyThrAsp 30
Db 1757 TACTCGATGGCGCAAGGAGCTCGGCGCGGAGTTCGGCGACCTGTGCAGGCAC 1816
Qy 31 ArgGluThrArgGluAlaLeuAlaCysLysSerIleSerLysArgLysLeuArgThrAla 50
Db 1817 CGGACGAGCGCGAGAGCTGGCTGCAAGCATCGCGAAGCGAAGCTGGCGGCCAGG 1876
Qy 51 ValAspValGluAppValArgGluValThrIleMetSerThrLeuProGluHisPro 70
Db 1877 GAGCAGCTGGAGCAGCTCGCGCGGAGGTGCAGATCATGCACCACTCTCGCGCCAGCCC 1936
Qy 71 AsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrValHisLeuValMetGlu 90
Db 1937 AACGTGTGGCGCTCCGCGCGCGCTACGAGACAAGCAGAGCGTGCACCTCGTCATGGAG 1996
Qy 91 LeuCysGluGlyGlyGluLeuPheGlyArgIleValAlaArgGlyHisTyrThrGluArg 110
Db 1997 CTGTGCGCGCGGGGAGCTTTCGACCGCATCATCGCGCGGGCCAGTACACGAGGCGC 2056
Qy 111 AlaAlaAlaThrValAlaAlaArgThrIleAlaGluValValArgMetCysHisValAsnGly 130
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Qy 131 ValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsnLysLysGluAsnSer 150
Db 2117 GTGATGACCGGGGAGCTCAAGCCGAGAACTTCTGCTGCTCAGCAGGAGGAGGAGCGG 2176
Qy 151 AlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysProGlyGluArgPheThr 170
Db 2177 CCGTCAAGGCGCCGACTTCGGCTCTCCGTCTTCTTCAAGGAGGCGAGCTGCTCAGG 2236
Qy 171 GluIleValGlySerProTyrTyrMetAlaProGluValLeuLysArgAsnTyrGlyPro 190
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Qy 263 ValLeu 264
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RESULT 4

US-08-459-444-26
; Sequence 26, Application US/08459444A
; Patent No. 6121014
; GENERAL INFORMATION:
; APPLICANT: Kozziel, Michael G.
; Desai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Lounis, Karen L.
; TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
; NUCLEIC ACID CODING SEQUENCE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,444A
; FILING DATE: 02-Jun-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/851,715
; FILING DATE: 25-SEP-1992
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4162 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1418..1427
; OTHER INFORMATION: /note= "start of mRNA"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1481..2366
; FEATURE:
; NAME/KEY: intron
; LOCATION: 2367..2451
; FEATURE:
; NAME/KEY: exon
; LOCATION: 2452..2602
; FEATURE:
; NAME/KEY: intron
; LOCATION: 2603..2690
; FEATURE:
; NAME/KEY: exon
; LOCATION: 2691..2804
; FEATURE:

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NAME/KEY: intron
LOCATION: 2805..2906
FEATURE:
NAME/KEY: exon
LOCATION: 2907..3075
FEATURE:
NAME/KEY: intron
LOCATION: 3076..3177
FEATURE:
NAME/KEY: exon
LOCATION: 3178..3304
FEATURE:
NAME/KEY: intron
LOCATION: 3305..3398
FEATURE:
NAME/KEY: exon
LOCATION: 3399..3498
FEATURE:
NAME/KEY: intron
LOCATION: 3499..3713
FEATURE:
NAME/KEY: exon
LOCATION: 3714..3811
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-08-459-444-26

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Alignment Scores:
Pred. No.: 9.45e-92 Length: 4162
Score: 792.50 Matches: 159
Percent Similarity: 66.67% Conservative: 29
Best Local Similarity: 56.38% Mismatches: 66
Query Match: 55.85% Indels: 29
DB: 3 Gaps: 1

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US-08-989-881-2 (1-274) x US-08-459-444-26 (1-4162)

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Qy 11 TyrIleuGlyArgGluLeuGlyArgGlyPheGlyIleThrTyrLeuCysThrAsp 30
Db 1757 TACTCGATGGCAAGGAGCTCGGGCGGGGAGTTCGGCGTGCAGCGACCTGTGCACGCAC 1816
Qy 31 ArgGluThrArgGluAlaLeuAlaCysIleSerIleSerIleArgGlyLeuArgThrAla 50
Db 1817 CGACGAGCGCGGAGAGCTGGGTGCAGACGATCGGAGCGGAGCTGGCGGCCAGG 1876
Qy 51 ValAspValGluAspValArgArgGluValThrIleMetSerThrLeuProGluHisPro 70
Db 1877 GAGGACGTGACGACGCGCGGGAGGTGCAGATCATGCACCACTCTCCGGCCAGCCC 1936
Qy 71 AsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrValHisLeuValMetGlu 90
Db 1937 AACGTGGTGGGCTTCGGCGCGGCTACGAGGACAGCAGCGTGCACCTCGTCATGGAG 1996
Qy 91 LeuCysGluGlyGlyGluLeuPheGlyArgIleValAlaArgGlyHisTyrThrGluArg 110
Db 1997 CTGTGCGCGGGGGGAGCTCTTCGACCGCATCATCGCCCGGGCCAGTACACGGAGCG 2056
Qy 111 AlaAlaAlaThrValAlaArgThrIleAlaGluValValArgMetCysHisValAsnGly 130
Db 2057 GGCGCGCGGAGCTGTGCGCGCATCGTGCAGATCGTGCACACCTGCCACTCCATGGGG 2116
Qy 131 ValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaLeuLysLysGluAsnSer 150
Db 2117 GTGATGCCCGGAGACATCAAGCCCGAGACTTCTGCTGCTCAGGAGGACGAGGAGCGG 2176
Qy 151 AlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysProGlyGluArgPheThr 170
Db 2177 CCCTCAAGGCCACCGACTTCGGCTCTCGTCTCTTCAAGGAGGCGGAGCTGCACGG 2236
Qy 171 GluIleValGlySerProTyrTyrMetAlaProGluValLeuLysArgAsnTyrGlyPro 190
Db 2237 GACATCGTCGGCAGCCCTACTACATCGCCCGGAGGTGTCAAGAGGAAAGTACGCGCCG 2296
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RESULT 5

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US-09-547-422-26

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; Sequence 26, Application US/09547422
; Patent No. 6320100
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; Desai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Lounis, Karen L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE

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```

NUMBER OF SEQUENCES: 94

```

```

CORRESPONDENCE ADDRESS:

```

```

ADDRESS: No. 6320100artis Agribusiness Biotechnology Research, Inc.

```

```

STREET: 3054 Cornwallis Road

```

```

CITY: Research Triangle Park

```

```

STATE: NC

```

```

COUNTRY: USA

```

```

ZIP: 27709

```

```

COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: Patent In Release #1.0, Version #1.30

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CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/09/547,422

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FILING DATE: 11-Apr-2000

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CLASSIFICATION: <Unknown>

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PRIOR APPLICATION DATA:

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APPLICATION NUMBER: US 08/459,595

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FILING DATE: 02-JUN-1995

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APPLICATION NUMBER: US 07/951,715

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FILING DATE: 25-SEP-1992

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```

APPLICATION NUMBER: US 07/772,027

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```

FILING DATE: 04-OCT-1991

```

```

ATTORNEY/AGENT INFORMATION:

```

```

NAME: Meigs, J. Timothy

```

```

REGISTRATION NUMBER: 38,241

```

```

REFERENCE/DOCKET NUMBER: S-18805H

```

```

TELECOMMUNICATION INFORMATION:

```

```

TELEPHONE: (919)541-8567

```

```

TELEFAX: (919)541-8689

```

```

INFORMATION FOR SEQ ID NO: 26:

```

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SEQUENCE CHARACTERISTICS:

```

LENGTH: 4162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1418..1427
OTHER INFORMATION: /note= "start of mRNA"
FEATURE:
NAME/KEY: exon
LOCATION: 1481..2366
FEATURE:
NAME/KEY: intron
LOCATION: 2367..2451
FEATURE:
NAME/KEY: exon
LOCATION: 2452..2602
FEATURE:
NAME/KEY: intron
LOCATION: 2603..2690
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NAME/KEY: exon
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NAME/KEY: intron
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NAME/KEY: exon
LOCATION: 3399..3498
FEATURE:
NAME/KEY: intron
LOCATION: 3499..3713
FEATURE:
NAME/KEY: exon
LOCATION: 3714..3811
SEQUENCE DESCRIPTION: SEQ ID NO: 26:

US-09-547-422-26

Alignment Scores:
Pred. No.: 9,45e-92 Length: 4162
Score: 792.50 Matches: 159
Percent Similarity: 66.67% Conservative: 29
Best Local Similarity: 56.38% Mismatches: 66
Query Match: 55.85% Indels: 29
DB: 3 Gaps: 1

US-08-989-881-2 (1-274) x US-09-547-422-26 (1-4162)

Qy 11 TyrileuGlyArgGluLeuGlyArgGlyGluPheGlyIleThrTyLeuCysThrAsp 30
Db 1757 TACTCGATGGCGAAGAGCTCGGCGCGGAGTTCCGGCTGCAAGAGCGGAAGCTGGCGCCAGG 1876
Qy 31 ArgGluThrArgGluAlaLeuAlaCysLysSerIleSerLysArgLysLeuArgThrAla 50
Db 1817 CGGACGCGCGGAGAGCTGGCTGCGAGATCGCAAGCGGAAGCTGGCGCCAGG 1876
Qy 51 ValAspValGluAspValArgGluValThrIleMetSerThrLeuProGluHisPro 70
Db 1877 GAGGACGTGGACGACGTGGCGCGGAGGTGCAGATCATGCACACCTCTCCGCGCGAGGCC 1936

Qy 71 AsnValValLysLeuLysLeuAlaThrTyGluAspAsnGluThrValHisLeuValMetGlu 90
Db 1937 AACGTGGTGGGCTCCGCGCGCGTACGAGGACGAGCGTGCACCTCTCGTCTAGGAG 1996
Qy 91 LeuCysGluGlyGlyGluLeuPheGlyArgIleValAlaArgGlyHisTyThrGluArg 110
Db 1997 CTGTGCGCGGGGGAGCTCTTCACCGCATCATCGCCCGGGGCGAGTACACGAGCGC 2056
Qy 111 AlaAlaThrValAlaArgThrIleAlaGluValValArgMetCysHisValAsnGly 130
Db 2057 GCGCGCGGAGCTGTGCGCGCATCTGTGAGATCGTCACACCTGCACCTCCATCCATGGG 2116
Qy 131 ValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsnLysLysGluAsnSer 150
Db 2117 GTGATGCACCGGACATCAAGCCGAGAACTTCTGTGCTGCAGAGGACGAGACGCG 2176
Qy 151 AlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysProGlyLysArgPheThr 170
Db 2177 CCGCTCAAGGCCACCGACTTCGGCTCTCCGCTCTTCTCAAGGAGGCGAGCTGCTCAGG 2236
Qy 171 GluIleValGlySerProTyTyMetAlaProGluValLeuLysArgAsnTyThrGlyPro 190
Db 2237 GACATCGTCGCGCAGCGCTACTACATCGCGCCGAGGTGCTCAAGAGGAAGTACGCGCGC 2296
Qy 191 GluValAspValTrpSerAlaGlyValIleLeuTyIleLeuLeuCysGlyValProPro 210
Db 2297 GAGCCGACATCTGGAGCGTGCAGCTCATGTCTACATCTTCTCGCGCGGCTGCTCC 2356
Qy 211 PheTrpAla----- 213
Db 2357 TTCTGGGC-AGGTCGGATCCGTCGCTGTTCTCTAGACGATATACAGACCCGACGATG 2415
Qy 214 -----GluThrGluGlnGlyValAlaLeuAla 222
Db 2416 GATTTGCTTCTCAGCCCTGTTCTTTCATCACAGAGAAGAGACGCGATCTTCACCGCC 2475
Qy 223 IleLeuArgGlyValLeuAspPheLysArgAspProTrpSerGlnIleSerGluSerAla 242
Db 2476 ATCTGCGAGGCGAGCTTGACCTCTCAGCGAGCGATGCGCCACACATCTCCGCGGAGCC 2535
Qy 243 LysSerLeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGlnGln 262
Db 2536 AAGGATCTCTCAGAGAGATGCTCAACATCAACCCCAAGGAGCGGCTCACGGCGTCCAG 2595
Qy 263 ValLeu 264
Db 2596 GTCCTC 2601

RESULT 6

US-09-988-462-26
; Sequence 26, Application US/09988462
; Patent No. 6720488

GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.

Desai, Nalini M.
Lewis, Kelly S.

Kramer, Vance C.
Warren, Gregory W.

Evola, Stephen V.
Crossland, Lyle D.

Wright, Martha S.
Merlin, Ellis J.

Lauis, Karen L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:

ADDRESSEE: Syngenta Biotechnology, Inc.
STREET: 3054 Cornwallis Road

CITY: Research Triangle Park
STATE: NC

COUNTRY: USA

[illegible]

Db 2175 CGCTCAAGGCCACCGACTTCGGCCCTCTCGCTTCTTCAAGGAGCGGAGCTGCTCAGG 2234
Qy 171 GluValValGlySerProTyrTyrMetAlaProGluValLeuLysArgAsnTyrGlyPro 190
Db 2235 GACATGTCGGCAGCGCTTACTACATCGCGCCGAGGTGCTCAAGAGGAAGTACGGCCG 2294
Qy 191 GluValAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeuCysGlyValPro 210
Db 2295 GAGCGCGACATCGGAGCGTCGGCGTCTATCATCTTCTCGCGCGTGCCTCC 2354
Qy 211 PheTrpAla----- 213
Db 2355 TTCTGGGC-AGTTCGGATCGTCCGTCGTCCTAGACGATATACAGACCGGACGATG 2413
Qy 214 -----GluThrGluGlnGlyValAlaLeuAla 222
Db 2414 GATTTCCTTCTCAGCCCTGTTCTTTCATCACCAGAGACGAGACGGCATCTTCACCGCC 2473
Qy 223 IleLeuArgGlyValLeuAspPheLysArgAspProTyrTrpSerGlnIleSerGluSerAla 242
Db 2474 ATCCCTCGAGGCGAGCTTCACTCTCCAGCGAGCCATGGCCACACATCTCGCGGGAGCC 2533
Qy 243 LysSerLeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGlnGln 262
Db 2534 AAGGATCTCGTCAAGAGATGCTCAACATCAACCCCAAGAGCGGCTCAGCGGTTCCAG 2593
Qy 263 ValLeu 264
Db 2594 GTCCCTC 2599

RESULT 8

US-07-951-715A-20
Sequence 20, Application US/07951715A
Patent No. 5625136

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/951,715A
FILING DATE: 25-SEP-1992
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8615
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 3..1226 /note= "cDNA sequence for maize
OTHER INFORMATION: pollen-specific calcium dependent protein kinase gene as
OTHER INFORMATION: disclosed in Figure 30."
US-07-951-715A-20

Alignment Scores:

Pred. No.: 2,158-80 Length: 1349
Score: 599.00 Matches: 132
Percent Similarity: 73.68% Conservative: 22
Best Local Similarity: 63.16% Mismatches: 55
Query Match: 49.26% Indels: 0
DB: 1 Gaps: 0

US-08-989-881-2 (1-274) x US-07-951-715A-20 (1-1349)

Qy 62 IleMetSerThrLeuProGluHisProAsnValValLysLeuLysAlaThrTyrGluAsp 81
Db 6 ATCATGACCACTCTCCGGCCAGCCCAACGCTGGTGGCCCTCCGGCGCGCTACGAGGAC 65
Qy 82 AsnGluThrValHisLeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArgIle 101
Db 66 AAGCAGAGCGTGCACCTGCTCATGGAGCTGTGCGCGCGGGAGCTCTTTCAGCCGCATC 125
Qy 102 ValAlaArgGlyHisTyrThrGluArgAlaAlaThrValAlaArgThrIleAlaGlu 121
Db 126 ATCCGCCGGGCGCAGTACACGAGCGCGCGCGCGGAGCTGCTCGCGCCCATCTGCAG 185
Qy 122 ValValArgMetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAsnPhe 141
Db 186 ATCGTGCACACCTGCCACTCCATGGGGGTGATGACCGGGACATCAAGCCCGAGAACTTC 245
Qy 142 LeuPheAlaAsnLysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerVal 161
Db 246 CTGCTGCTCAAGCAAGGAGGAGGACGCGCGCTCAAGCGCCACCGACTTCGGCTCTCCGTC 305
Qy 162 LeuPheLysProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAlaPro 181
Db 306 TTCITCAAGGAGGCGAGCTGCTCAGGACATCTGTCGCGAGCGCTACTACATCGCGCCC 365
Qy 182 GluValLeuLysArgAsnTyrGlyProGluValAspValTrpSerAlaGlyValIleLeu 201
Db 366 GAGGTGCTCAAGAGGAAGTACGGCCGCGGAGCGGCACATCTGGAGCGTCTGCGCTCATGCTC 425
Qy 202 TyrIleLeuLeuCysGlyValProPheThrAlaGluThrGluGlnGlyValAlaLeu 221
Db 426 TACATCTTCTCCGCGCGTGCCTCCCTTCTGGGCGAGAGACGAGAACGGCATCTTCACC 485
Qy 222 AlaIleLeuArgGlyValLeuAspPheLysArgAspProTyrTrpSerGlnIleSerGluSer 241
Db 486 GCCATCTTCGCGAGGCGAGCTTGACCTCTCCAGCGCCATGGCCACACATCTTCGCGCGGA 545
Qy 242 AlaLysSerLeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGln 261
Db 546 GCCAAGGATCTCGTCAAGAGATGCTCAACATCAACCCCAAGAGCGGCTTCAGCGCGTTC 605

Qy 262 GlnValLeuAspHisProTyrPheGln 270
Db 606 CAGGTCTCAATCAACCCATGGATCAAA 632

RESULT 9

US-08-459-448A-20
; Sequence 20, Application US/08459448A
; Patent No. 5859336

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lytle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 5859336artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA

ZIP: 10591-9005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,448A

FILING DATE: 02-JUN-1995

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Pace, Gary M.

REGISTRATION NUMBER: 40403

REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8582

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 1349 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 3..1226

OTHER INFORMATION: /note= "cDNA sequence for maize

OTHER INFORMATION: pollen-specific calcium dependent protein kinase gene as

OTHER INFORMATION: disclosed in Figure 30."

US-08-459-448A-20

Alignment Scores:

Pred. No.: 2.15e-80 Length: 1349
Score: 699.00 Matches: 132
Percent Similarity: 73.68% Conservative: 22
Best Local Similarity: 63.16% Mismatches: 55
Query Match: 49.26% Indels: 0
DB: 2 Gaps: 0

US-08-989-881-2 (1-274) x US-08-459-448A-20 (1-1349)

Qy 62 ILeMetSerThrLeuProGluHisProAsnValVallyLeuLysLeuAlaThrTyrGluAsp 81
Db 6 ATCATGCACCACTCTCCGCCAGCCCAACCTGTGTGGCCCTCCGGCGCGTACAGGAC 65
Qy 82 AsnGluThrValHisLeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArgIle 101
Db 66 AAGCAGAGCGTGCACCTCGTCATCGAGCTGTCCCGGGGGGAGCTCTTCGACCGCATC 125
Qy 102 ValAlaArgGlyHisTyrThrGluArgAlaAlaAlaThrValAlaArgThrIleAlaGlu 121
Db 126 ATCCCGCGGGCCAGTACACGAGCGCGCGCGCGAGCTGTCCCGGGGGGAGCTCTTCGACCGCATC 185
Qy 122 ValValArgMetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAsnPhe 141
Db 186 ATCGTGCACACCTGCCACTCCATCGGGGTGATGACCGGGGACATCAAGCCGAGAACATTC 245
Qy 142 LeuPheAlaAsnLysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerVal 161
Db 246 CTGCTGCTCAGCAAGGAGGAGCGCGCGCTCAAGGCCACCGACTTCGGCTCTCCGTC 305
Qy 162 LeuPheLysProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAlaPro 181
Db 306 TTCTTCAAGGAGGCGAGCTGCTCAGGGACATCTCGCGAGCGCTACTACTATCGCGCC 365
Qy 182 GluValLeuLysArgAsnTyrGlyProGluValAspValTyrSerAlaGlyValIleLeu 201
Db 366 GAGGTGCTCAAGAGGAAGTACGGCCCGGAGCCGACATCTGGAGCGTCCGGCTCATGCTC 425
Qy 202 TyrIleLeuLysCysGlyValProPheTrpAlaGluThrGluGlnGlyValAlaLeu 221
Db 426 TACATCTCTCGCGCGGTGCTCTCTTCTGGCAGAGAACGAGACGGCATCTTCACC 485
Qy 222 AlaIleLeuArgGlyValLeuAspPheLysArgAspProTrpSerGlnIleSerGluSer 241
Db 486 GCCATCTCGCAGGCGAGCTTACCTCTCCAGCGAGCATGGCCACACATCTCGCGCGGA 545
Qy 242 AlalysSerLeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGln 261
Db 546 GCCAAGGATCTCGTCAAGAAAGATGCTCAACATCAACCCCAAGGAGCGGCTCACGGCGTTC 605
Qy 262 GlnValLeuAspHisProTyrPheGln 270
Db 606 CAGGTCTCAATCAACCCATGGATCAAA 632

RESULT 10

US-08-459-595A-20

; Sequence 20, Application US/08459595A

; Patent No. 6018104

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lytle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.

CLASSIFICATION:
PRIOR APPLICATION DATA: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 3..1226
OTHER INFORMATION: /note= "cDNA sequence for maize
OTHER INFORMATION: pollen-specific calcium dependent protein kinase gene as
OTHER INFORMATION: disclosed in Figure 30."

US-08-459-504B-20

Alignment Scores:
Pred. No.: 2,158-80 Length: 1349
Score: 699.00 Matches: 132
Percent Similarity: 73.68% Conservative: 22
Best Local Similarity: 63.16% Mismatches: 55
Query Match: 49.26% Indels: 0
DB: 3 Gaps: 0

US-08-989-881-2 (1-274) x US-08-459-504B-20 (1-1349)

Qy 62 IleMetSerThrLeuProGluHisProAsnValValLysLeuLysAlaThrTyrGluAsp 81
Db ATATGACACCTCTCCGGCCAGCCCAAGTGTGGGCTCCGGGGCGGTACAGGAC 65
Qy 82 AsnGluThrValHisLeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArgile 101
Db AAGCAGACGCTGCCTCTCATGAGCTGTGCGCGGGGAGCTCTTCGACCGCATC 125
Qy 102 ValAlaArgGlyHisTyrThrGluArgAlaAlaAlaThrValAlaArgThrIleAlaGlu 121
Db ATCGCCGGGGCCAGTACACGAGCGCGCGCGGAGCTGCTCGCGGCCATCGTGAG 185
Qy 122 ValValArgMetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAsnPhe 141
Db ATGTGACACCTGCATCTCCATGCGGTGTATGACCGGACATCAAGCCCGAGAACTTC 245
Qy 142 LeuPheAlaAsnLysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerVal 161
Db CTGCTGCTCAGCAGGAGGAGCGCGCGCTCAAGGCCACCGACTTCGGCTCTCCGTC 305
Qy 162 LeuPheLysProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAlaPro 181
Db TTCTTCAAGGAGGGCGAGCTGTCTCAGGGACATCGTCGCGAGCGGCTACTACATCGCGCC 365
Qy 182 GluValLeuLysArgAsnTyrGlyProGluValAspValTyrSerAlaGlyValIleLeu 201
Db GAGTGTCTCAGAGAGAGTACGGCCCGAGGCGGACATCTGGAGCGTGGGTCTATGCTC 425
Qy 202 TyrIleLeuLysCysGlyValProProPheThrAlaGluThrGluGlnGlyValAlaLeu 221
Db TACATCTCTCTCGCGGGGTGCTCTCTCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAG 485

Qy 222 AlaIleLeuArgGlyValValLeuAspPheLysArgAspProTyrSerGlnIleSerGluSer 241
Db GCCATCTCGCGAGGCGACCTTGACCTCTCCAGCGAGCGCATGGCCACACATCTCGCGCGGA 545
Qy 242 AlaLysSerLeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGln 261
Db GCCAAGGATCTCGTCAAGAAGATGCTCAACATCAACCCCAAGAGCGGCTCAGCGGCTTC 605
Qy 262 GlnValLeuAspHisProTyrIleGln 270
Db CAGGTCTCTCAATCACCCTGATGATCAAA 632

RESULT 12

US-08-459-444-20

Sequence 0, Application US/08459444A

Patent No. 6121014

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.

Desai, Nalini M.

Lewis, Kelly S.

Kramer, Vance C.

Warren, Gregory W.

Evola, Stephen V.

Crossland, Lyle D.

Wright, Martha S.

Merlin, Ellis J.

Lauis, Karen L.

TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED

NUCLEIC ACID CODING SEQUENCE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,444A

FILING DATE: 02-Jun-1995

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8587

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: /note= "cDNA sequence for maize

pollen-specific calcium dependent protein kinase gene a

disclosed in Figure 30."

SEQUENCE CHARACTERISTICS:

LENGTH: 1349 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 3..1226

SEQUENCE DESCRIPTION: SEQ ID NO: 20:

US-08-459-444-20

Alignment Scores: 2,15e-80 Length: 1349
Pred. No.: 699,00 Matches: 132
Score: 73.68% Conservative: 22
Percent Similarity: 63.16% Mismatches: 55
Best Local Similarity: 49.26% Indels: 0
Query Match: 3 Gaps: 0
DB:

US-08-989-881-2 (1-274) x US-08-459-444-20 (1-1349)

QY 62 IleMetSerThrLeuProGluHisProAsnValValLysLeuLysAlaThrTyrGluAsp 81
DB 6 ATCATGACACCTCTCCGCGCCAGCCCAACGTGTGGGCTCCGCGCGGTACGAGGAC 65
QY 82 AsnGluThrValHisLeuValMetGluLeuLeuGlyGlyGlyGlyGlyGlyGlyGly 101
DB 66 AAGCAGAGCGTGACCTCGTCATGGAGCTGTGCGCGGGCGGGAGCTCTTCGACCGCATC 125
QY 102 ValAlaArgGlyHisTyrThrGluA:GAlaAlaThrValAlaAlaArgThrIleAlaGlu 121
DB 126 ATCGCGCGGGCCAGTACACGAGCGCGCGCGCGAGCTGTGCGCGGCATCTGTCGAC 185
QY 122 ValValArgMetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAsnPhe 141
DB 186 ATCGTGCACACCTGCCACTCTATGGGGGTGATGACCGGGACATCAAGCCCGAGAACTTC 245
QY 142 LeuPheAlaAsnLysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerVal 161
DB 246 CTGCTCTCAGCAGGAGGAGCGCGCGCTCAAGGCCACCGACTTCGGCTCTCTCGTC 305
QY 162 LeuPheLysProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAlaPro 181
DB 306 TTCTTCAAGGAGGCGAGCTGTCTCAGGACATCTCGGACGCGCTACTACATCGCGGCC 365
QY 182 GluValLeuLysArgAsnTyrGlyProGluValAspValTrpSerAlaGlyValIleLeu 201
DB 366 GAGTGCTCAAGAGGAAGTACGCGCGCGCGGCGGACATCTGGAGCGTGGCGGTCTGTC 425
QY 202 TyrIleLeuLeuCysGlyValProProPheTrpAlaGluThrGluGlnGlyValAlaLeu 221
DB 426 TACATCTCTCGCGCGGTGCTCTCTCTCTGCGGAGAGACGAGACCGCATCTTCACC 485
QY 222 AlaIleLeuArgGlyValLeuAspPheLysArgAspProTrpSerGlnIleSerGluSer 241
DB 486 GCCATCTCGGAGGCGAGCTTGACCTCTCCAGCGAGCCATGCGCCACACATCTCGCGGGA 545
QY 242 AlaLysSerLeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGln 261
DB 546 GCCAAGGATCTCTCAAGAGATGCTCAACATCAACCCCAAGGAGCGGTTCACGGGTTTC 605
QY 262 GlnValLeuAspHisProTrpIleGln 270
DB 606 CAGGTCTCAATCAACCCATGATCAAA 632

RESULT 13

US-09-547-422-20
Sequence 0, Application US/09547422
Patent No. 6320100
GENERAL INFORMATION:

APPLICANT: Kozziel, Michael G.

Desai, Nalini M.

Lewis, Kelly S.

Kramer, Vance C.

Warren, Gregory W.

Evola, Stephen V.

Crossland, Lyle D.

Wright, Martha S.

Merlin, Ellis J.

Lauis, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6320100artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/547,422

FILING DATE: 11-Apr-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/459,595

FILING DATE: 02-JUN-1995

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: S-18805H

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8587

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: /note= "cDNA sequence for maize

pollen-specific calcium dependent protein kinase gene as

disclosed in Figure 30."

SEQUENCE CHARACTERISTICS:

LENGTH: 1349 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 3..1226

SEQUENCE DESCRIPTION: SEQ ID NO: 20:

US-09-547-422-20

Alignment Scores:

Pred. No.: 2,15e-80 Length: 1349
Score: 699,00 Matches: 132
Percent Similarity: 73.68% Conservative: 22
Best Local Similarity: 63.16% Mismatches: 55
Query Match: 49.26% Indels: 0
DB: 3 Gaps: 0

US-08-989-881-2 (1-274) x US-09-547-422-20 (1-1349)

QY 62 IleMetSerThrLeuProGluHisProAsnValValLysLeuLysAlaThrTyrGluAsp 81
DB 6 ATCATGACACCTCTCCGCGCCAGCCCAACGTGTGGGCTCCGCGCGGTACGAGGAC 65
QY 82 AsnGluThrValHisLeuValMetGluLeuCysGlyGlyGlyGlyGlyGlyGlyGly 101
DB 66 AAGCAGAGCGTGACCTCGTCATGGAGCTGTGCGCGGGCGGGAGCTCTTCACCGCATC 125
QY 102 ValAlaArgGlyHisTyrThrGluArgAlaAlaThrValAlaAlaArgThrIleAlaGlu 121
DB 126 ATCGCGCGGGCCAGTACACGAGCGCGCGCGAGCTGTGCGCGGCATCTGTCGAC 185
QY 122 ValValArgMetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAsnPhe 141
DB 186 ATCGTGCACACCTGCCACTCTCCATGGGGGTGATGACCGGGACATCAAGCCCGAGAACTTC 245

Qy 142 LeuPhealaAsnLysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerVal 161
Db 246 CTGCTGCTCAGCAAGGACGAGCGCGCTCAAGGCCACCGACTTCGGGCTCTCCGTC 305
Qy 162 LeuPheLysProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAlaPro 181
Db 306 TTCCTCAAGAGGAGGAGCTGCTCAGGACATCGTCGCGAGCGCTACTACATCGCGCC 365
Qy 182 GluValLeuLysArgAsnTyrGlyProGluValAspValTyrSerAlaGlyValIleLeu 201
Db 366 GAGGTGCTCAAGAGGAGTACGGCGCGGAGCGGACATCTCGAGCGTCTGGGCTCATGTC 425
Qy 202 TyrIleLeuLeuCysGlyValProPheThrAlaGluThrGluGlnGlyValAlaLeu 221
Db 426 TACATCTTCCTCGCGCGGCTGCTCCCTCTGGGAGAGAACGAGACGGCATCTTACC 485
Qy 222 AlaIleLeuArgGlyValLeuAspPheLysArgAspProTyrSerGlnIleSerGluSer 241
Db 486 GCCATCTCGAGGAGGAGCTTGACCTCTCCAGCGGACATGCGCACACATCTCGCGGGA 545
Qy 242 AlalysSerLeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGln 261
Db 546 GCCAAGGATCTCGTCAAGAGATGCTCAACATCAACCCCAAGGAGCGGCTCACGCGGTC 605
Qy 262 GlnValLeuAspHisProTyrIleGln 270
Db 606 CAGGTCTCTCAATCAATCAATGATCAAA 632

RESULT 14

US-09-988-462-20

; Sequence 20, Application US/09988462

; Patent No. 6720488

; GENERAL INFORMATION:

; APPLICANT: Koziel, Michael G.

; Desai, Nalini M.

; Lewis, Kelly S.

; Kramer, Vance C.

; Warren, Gregory W.

; Evola, Stephen V.

; Crossland, Lyle D.

; Wright, Martha S.

; Merlin, Ellis J.

; Launig, Karen L.

; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

; INSECTICIDAL ACTIVITY IN MAIZE

; NUMBER OF SEQUENCES: 94

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Syngenta Biotechnology, Inc.

; STREET: 3054 Cornwallis Road

; CITY: Research Triangle Park

; STATE: NC

; COUNTRY: USA

; ZIP: 27709

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/988,462

; FILING DATE: 20-NOV-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 09/547,422

; FILING DATE: 11-APR-2000

; APPLICATION NUMBER: US 08/459,504

; FILING DATE: 02-JUN-1995

; APPLICATION NUMBER: US 07/951,715

; FILING DATE: 25-SEP-1992

; APPLICATION NUMBER: US 07/772,027

; FILING DATE: 04-OCT-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Meigs, J. Timothy

; REGISTRATION NUMBER: 38,241

; REFERENCE/DOCKET NUMBER: S-188051

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (919)541-8587

; TELEFAX: (919)541-8689

; INFORMATION FOR SEQ ID NO: 20:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1349 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 3..1226

; OTHER INFORMATION: /note="cDNA sequence for maize

; pollen-specific calcium dependent protein kinase gene as

; disclosed in Figure 30."

; SEQUENCE DESCRIPTION: SEQ ID NO: 20:

; US-09-988-462-20

Alignment Scores:

Pred. No.: 2.15e-80 Length: 1349

Score: 699.00 Matches: 132

Percent Similarity: 73.68% Conservative: 22

Best Local Similarity: 63.16% Mismatches: 55

Query Match: 49.26% Indels: 0

DB: 4 Gaps: 0

US-08-989-881-2 (1-274) x US-09-988-462-20 (1-1349)

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Db 6 ATCATGCACACCTCTCCGCCAGCCCAACGTGTGGGCTTCCCGCGCGCTACGAGGAC 65
Qy 82 AsnGluThrValHisLeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArgIle 101
Db 66 AAGCAGAGCGTGCACCTCTGTCATGGAGCTGTGCGGCGCGGGAGCTCTTCGACCGCATC 125
Qy 102 ValAlaArgGlyHisTyrThrGluArgAlaAlaAlaThrValAlaLeaThrIleAlaGlu 121
Db 126 ATCCCGCGGCGGCGAGTACACGAGCGCGCGCGGAGTGTGTCGCGCCATCGTCGAG 185
Qy 122 ValValArgMetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAsnPhe 141
Db 186 ATCGTGACACCTGCCACTCCATGGGGTGATGCACCGGACATCAAGCCGAGAACTTC 245
Qy 142 LeuPheAlaAsnLysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerVal 161
Db 246 CTGCTGCTCAGCAAGGACGAGGACCGCGCTCAGGCCACCGACTTCGGGCTCTCCGTC 305
Qy 162 LeuPheLysProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAlaPro 181
Db 306 TTCCTCAAGGAGGCGAGCTGCTCAGGACATCGTCGCGAGCGCTACTACATCGCGCC 365
Qy 182 GluValLeuLysArgAsnTyrGlyProGluValAspValTyrSerAlaGlyValIleLeu 201
Db 366 GAGGTGCTCAAGAGGAAAGTACGGCGCGGAGCGACATCTGGAGCGTCTGGGCTCATGTC 425
Qy 202 TyrIleLeuLeuCysGlyValProPheThrAlaGluThrGluGlnGlyValAlaLeu 221
Db 426 TACATCTTCCTCGCGCGGCTGCTCCCTCTGGGAGAGAACGAGACGGCATCTTACC 485
Qy 222 AlaIleLeuArgGlyValLeuAspPheLysArgAspProTyrSerGlnIleSerGluSer 241
Db 486 GCCATCTCGAGGAGGAGCTTGACCTCTCCAGCGGACATGCGCACACATCTCGCGGGA 545
Qy 242 AlalysSerLeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGln 261
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Qy 262 GlnValLeuAspHisProTyrIleGln 270

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US-09-347-801-3
; Sequence 3, Application US/09347801
; Patent No. 6262345
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/347,801
; CURRENT FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: 60/092,438
; EARLIER FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 3
; LENGTH: 2374
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-347-801-3

Alignment Scores:
Pred. No.:      9 51e-80      Length:      2374
Score:          697.00      Matches:      137
Percent Similarity: 65.06%      Conservative: 38
Best Local Similarity: 50.93%      Mismatches: 90
Query Match:      49.12%      Indels:      4
DB:                3      Gaps:      2

US-08-989-881-2 (1-274) x US-09-347-801-3 (1-2374)

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Qy      30 AspArgGluThrArg-----GluAlaLeuAlaCysLysSerIleSerLysArgLys 46
Db      765 GTCAAGAGGGCGAGTACAGGACAGACCGTCGCGCTCAAGATCATCGCCAAAGCTAAG 824
Qy      47 LeuArgThrAlaValAspValArgGluLeuPheGlyValThrIleMetSerThrLeu 66
Db      825 ATGACAACGCGCATATCCATTGAGGATGTCGTAGAGAGTAAATTTTGAGAGCGTTA 884
Qy      67 ProGluHisProAsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrValHis 86
Db      885 TCAGGGCACAAATAATCTCGTCAAAATTCATGATGCATGTGAGGATGCGCTCAATGTCTAC 944
Qy      87 LeuValMetGluLeuGlyGlyGlyGluLeuPheGlyValIleValAlaArg---Gly 105
Db      945 ATTGTGATGGAATTATGTGAGGAGGAGAAATTCCTAGACAGAAATATTAGCCAGAGCGGG 1004
Qy      106 HisTyrThrGluArgAlaAlaThrValAlaArgThrIleAlaGluValValArgMet 125
Db      1005 AGATACACAGAGGAAGATGCCAAAGCGATTGTTGTACAGATTTTGAGCGTAGTGCCTTC 1064
Qy      126 CysHisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsn 145
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Qy      146 LysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysPro 165
Db      1125 AGGGATGAAATAAGTCTCCCATGAAGATTGATTGATTTTGGTCTCTCTGATTTTCATTAGACCA 1184
Qy      166 GlyGluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluValLeuLys 185
Db      1185 GATGAAAGGCTTAATCATATTTGGAAGTGCATATTATGTTGCCCCACAGAGTTTTCAC 1244
Qy      186 ArgAsnTyrGlyProGluValAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeu 205
Db      1245 AGATCATATAGTATGGAAGCAGACATTTGGAGTATAGGTGTGCATAACGTAACGTAACGTC 1304
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Search completed: October 14, 2005, 17:14:24
Job time : 194 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 14, 2005, 17:02:14 : Search time 756 Seconds
(without alignments)
2540.626 Million cell updates/sec

Title: US-08-989-881-2

Perfect score: 1419

Sequence: 1 MANQIQISKYILGRELGRG.....TKRLTAQQVLDHPWQNAKK 274

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 8755912 seqs, 3504951483 residues

Total number of hits satisfying chosen parameters: 17531824

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40 cdi -LIST=45 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US08989881@cgn_1_1.886@runat_14102005_112731_5122
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOC=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-Fgapop=6 -Fgapext=7 -Ygapop=10 -Ygapext=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

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10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1419	100.0	1020	17	US-10-243-581B-5	Sequence 5, Appli
2	1322	93.2	1638	9	US-09-938-842A-1859	Sequence 1859, Ap
3	1322	93.2	1638	11	US-09-938-842A-1859	Sequence 1859, Ap
4	1252	88.2	2628	18	US-10-424-599-37843	Sequence 37843, A
5	1246	87.8	1787	18	US-10-425-114-10952	Sequence 10952, A
6	1164	82.0	2126	18	US-10-424-599-57457	Sequence 57457, A
7	1155	81.4	1978	19	US-10-437-963-7404	Sequence 7404, Ap
8	1147	80.8	2149	18	US-10-425-114-34236	Sequence 34236, A
9	1143	80.5	2244	18	US-10-425-114-28411	Sequence 28411, A
10	1143	80.5	2298	20	US-10-425-115-28928	Sequence 28928, A
11	1136	80.1	1974	18	US-10-425-114-24006	Sequence 24006, A
12	1136	80.1	2076	18	US-10-425-114-33866	Sequence 33866, A
13	1136	80.1	2131	20	US-10-425-115-13710	Sequence 13710, A
14	1135	80.0	1388	19	US-10-767-701-13220	Sequence 13220, A
15	1132	79.8	1770	17	US-10-260-238-574	Sequence 574, App
16	1132	79.8	1859	19	US-10-437-963-58337	Sequence 58337, A
17	1127	79.4	1602	9	US-09-938-842A-2304	Sequence 2304, Ap
18	1127	79.4	1602	11	US-09-938-842A-2304	Sequence 2304, Ap
19	1124	79.2	1868	22	US-10-510-871-91	Sequence 91, Appl
20	1115	78.6	2702	19	US-10-437-963-61474	Sequence 61474, A
21	1101	77.6	2054	18	US-10-425-114-32569	Sequence 32569, A
22	1101	77.6	4029	20	US-10-425-115-46503	Sequence 46503, A
23	1084	76.4	2387	19	US-10-437-963-56615	Sequence 56615, A
24	1071	75.5	960	17	US-10-260-238-5509	Sequence 5509, Ap
25	1064.5	75.0	2046	18	US-10-425-114-24849	Sequence 24849, A
26	1064.5	75.0	2068	18	US-10-425-114-32391	Sequence 32391, A
27	1062	74.8	1705	18	US-10-425-114-15775	Sequence 15775, A
28	1048	73.9	2048	20	US-10-425-115-29536	Sequence 29536, A
29	1041	73.4	2325	19	US-10-437-963-84309	Sequence 84309, A
30	1006	70.9	2642	18	US-10-424-599-11533	Sequence 11533, Ap
31	970	68.4	912	17	US-10-260-238-3517	Sequence 3517, Ap
32	947	66.7	2230	19	US-09-828-313-26	Sequence 26, Appl
33	947	66.7	2230	19	US-10-768-863A-26	Sequence 26, Appl
34	932	65.7	2714	19	US-10-437-963-39308	Sequence 39308, A
35	930	65.5	690	17	US-10-260-238-5765	Sequence 5765, Ap
36	930	65.5	690	22	US-10-481-032A-1186	Sequence 1186, Ap
37	926	65.3	1629	18	US-10-425-114-33660	Sequence 33660, A
38	926	65.3	2642	20	US-10-425-115-156016	Sequence 156016, A
39	921	64.9	1473	17	US-10-260-238-5645	Sequence 5645, Ap
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44	910	64.1	2050	18	US-10-425-114-10911	Sequence 10911, A
45	910	64.1	2147	18	US-10-425-114-13091	Sequence 13091, A

ALIGNMENTS

RESULT 1

US-10-243-581B-5
; Sequence 5, Application US/10243581B
; Publication No. US20030219763A1
; GENERAL INFORMATION:
; APPLICANT: Sheen, Jen
; TITLE OF INVENTION: Plant Protoplast Gene Expression Systems
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: 00786/386002
; CURRENT APPLICATION NUMBER: US/10/243 581B
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: PCT/US01/07999
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: US 60/189,074
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 08/989,881

;; PRIOR FILING DATE: 1997-12-12
;; PRIOR APPLICATION NUMBER: US 60/032,966
;; PRIOR FILING DATE: 1996-12-13
;; PRIOR APPLICATION NUMBER: US 09/371,338
;; PRIOR FILING DATE: 1999-08-10
;; PRIOR APPLICATION NUMBER: US 60/095,938
;; PRIOR FILING DATE: 1998-08-10
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 5
;; LENGTH: 1020
;; TYPE: DNA
;; ORGANISM: Arabidopsis thaliana
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (1)..(1020)
;; OTHER INFORMATION: N = a, t, c or g
US-10-243-581B-5

Alignment Scores:
Pred. No.: 1,01e-168 Length: 1020
Score: 1419.00 Matches: 274
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-08-989-881-2 (1-274) x US-10-243-581B-5 (1-1020)

Qy 1 MetAlaAsnGlnThrGlnIleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGly 20
Db 97 ATGGCTAATCAAACTCAGATCAGCGAAGTACATCTTAGACGAGAACTCGGTGCGGCG 156
Qy 21 GluPheGlyIleThrTyrLeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLys 40
Db 157 GAATTCGGATCAGGTATCTTTGTACAGATAGAGAGACTCGTGAAGCTTTAGCTTGC 216
Qy 41 SerIleSerLysArgLysLeuArgThrAlaValAspValGluAspValArgGluVal 60
Db 217 TCAATCTCCAGAGAAAGCTCCGAACCGCGTCGATGTGAAGACGTCCTCGTGAAGTC 276
Qy 61 ThrIleMetSerThrLeuProGluHisProAsnValValLysLeuLysAlaThrTyrGlu 80
Db 277 ACGATCATGCAACTTTACCGGACACCCAAACGTTGTGAACCTTAAGCGACTTATGAG 336
Qy 81 AspAsnGluThrValHisLeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArg 100
Db 337 GATAACCGAGACCGTGCATCTTTGTGATGGAGCTTTGTGAAGAGGTGAGCTTTTGTG 396
Qy 101 IleValAlaArgGlyHisTyrThrGluArgAlaAlaAlaThrValAlaArgThrIleAla 120
Db 397 ATTGTTCCAAAGAGGACATTTACAGAGCGTGCAGCGGCTACCGTCCGCGAAGCATCG 456
Qy 121 GluValValArgMetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAsn 140
Db 457 GAAGTTGTGAGGATGTGTCAATGTTGTTATGATAGATAGATTGGAAGCTTGAAGAT 516
Qy 141 PheLeuPheAlaLeuLysLysGluAsnSerAlaLeuLysAlaLeuAspPheGlyLeuSer 160
Db 517 TTCTTGTGTTGCTTAACAAGAGGAGAAATCTGCACTTAAGGCTATTGATTGTTGTTATCT 576
Qy 161 ValLeuPheLysProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAla 180
Db 577 GTTCTCTTTAAACCTTGAGAGAGGTTTACAGAGATTTGTTGAAGTCTCTTATTATATG 636
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Qy 201 LeuTyrIleLeuLeuCysGlyValProPheThrPalaGluThrGluGlnGlyValAla 220
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Qy 241 SerAlaLysSerLeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAla 260
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Db 877 CAGCAAGTCTTGTGATCACCTTGGATACAGAAATGCAAGAA 918

RESULT 2

US-09-938-842A-1859
; Sequence 1859, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1859
; LENGTH: 1638
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1859

Alignment Scores:

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Score: 1322.00 Matches: 253
Percent Similarity: 95.26% Conservative: 8
Best Local Similarity: 92.34% Mismatches: 13
Query Match: 93.16% Indels: 0
DB: 9 Gaps: 0

US-08-989-881-2 (1-274) x US-09-938-842A-1859 (1-1638)

Qy 1 MetAlaAsnGlnThrGlnIleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGly 20
Db 157 ATGAGCAATCAAACTCAGATCAGCGAAGTACATCTTAGTTCGTGAATTTAGGTCGAGGC 216
Qy 21 GluPheGlyIleThrTyrLeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLys 40
Db 217 GAATTCGGATCAGTACCTCTGTACTGATCGTGAACCCACGAGCTTTAGCTTGC 276
Qy 41 SerIleSerLysArgLysLeuArgThrAlaValAspValGluAspValArgGluVal 60
Db 277 TCGATTTCAAAGCGAAAGCTTCGAAACAGCTGTCGATATCGAAGACGCTTCGTCGAGGTA 336
Qy 61 ThrIleMetSerThrLeuProGluHisProAsnValValLysLeuLysAlaThrTyrGlu 80
Db 337 GCGATTATGTCTACTTTTACTGAGCATCCAAACGATGTTAAGCTTAAAGCTAGTTATGAG 396
Qy 81 AspAsnGluThrValHisLeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArg 100
Db 397 GATACCGAGAACTGCATCTGTTGAGCTTTGTAAGGAGGAGTCTTTTGTATCGG 456
Qy 101 IleValAlaArgGlyHisTyrThrGluArgAlaAlaAlaThrValAlaArgThrIleAla 120
Db 457 ATTGTTGCTAGAGGACATTTACCGGAGCGTGTGCTGCTGAGCTGTTGCGAAGACGATTGCT 516

QY 121 GluValValArgMetCysHisValAenGlyValMetHisArgAspLeuLysProGluAen 140
DB 517 GAGGTGTGATGATGTCTCACTAATGAGATTATGATCGAGATTGAAACCTGAGAT 576
QY 141 PheLeuPheAlaAasnLysLysGluAenSerAlaLeuLysAlaIleAspPheGlyLeuSer 160
DB 577 TTCTTGTGTCTAATAAAGAGAGATTCTCCACTAAAGGCTATTGATTTGGCTTGTCT 636
QY 161 ValLeuPheLysProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAla 180
DB 637 GTGTTCTTCAAAACCTGAGATAAGATTACAGAGATTGTAGGAAGTCGATTATATGCT 696
QY 181 ProGluValLeuLysArgAenTyrGlyProGluValAspValTyrSerAlaGlyValIle 200
DB 697 CCAGAAGTGTGAAGAGAGATTATGACAGGGTGTGTGGAGTCCCGGAGTTAT 756
QY 201 LeuTyrIleLeuLysCysGlyValProPheThrAlaGluThrGluGlnGlyValAla 220
DB 757 ATCTATATCTTGTCTGTGTCTCTCGGTTTGGGCTGAGACTGAACAGGTGTGCT 816
QY 221 LeuAlaIleLeuArgGlyValLeuAspPheLysArgAspProTyrSerGlnIleSerGlu 240
DB 817 CTGGCATCTTCCGGGAGTCTTGTGAAGCAGATGTTGGATCCTGATCCGACTAAGCGGTNACTGCT 876
QY 241 SerAlaLysSerLeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAla 260
DB 877 AGTGCAAGAGCTTGTGAAGCAGATGTTGGATCCTGATCCGACTAAGCGGTNACTGCT 936
QY 261 GlnGlnValLeuAspHisProTyrIleGlnAenAlaLysLys 274
DB 937 CAGCAAGTGTAGCTCACCCATGGATACAGAAATGCAAGAAA 978

RESULT 3

US-09-938-842A-1859
; Sequence 1859, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Krebs, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRI1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1859
; LENGTH: 1638
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1859

Alignment Scores:

Pred. No.: 3,65e-156 Length: 1638
Score: 1322.00 Matches: 253
Percent Similarity: 95.26% Conservative: 8
Best Local Similarity: 92.34% Mismatches: 13
Query Match: 93.16% Indels: 0
DB: 11 Gaps: 0

US-08-989-881-2 (1-274) x US-09-938-842A-1859 (1-1638)

QY 1 MetAlaAenGlnThrGlnIleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGly 20
DB 157 ATGAGCAATCAAACTCAGATCAGCGACAAATACATCTTAGTGTCGTGAATTAGTTCGAGGC 216

QY 21 GluPheGlyIleThrTyrLeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLys 40
DB 217 GAAATTCGGNATCACTTACTCTGTACTGATCGTGAAACCCAGAGCTTTAGCTTGCATA 276
QY 41 SerIleSerLysArgLysLeuArgThrAlaValAspValGluAspValArgArgGluVal 60
DB 277 TCGATTTCAAGCGAAAGCTTCGAACAGCTGTCGATATCGAAGAGCTTCTGCTGAGGTA 336
QY 61 ThrIleMetSerThrLeuProGluHisProAenValValLysLeuLysAlaThrTyrGlu 80
DB 337 CGGATTATGTCTTACTTACCTGAGCATCCAAACGCTAGTTAAGCTTAGTTATGAG 396
QY 81 AspAenGluThrValHisLeuValMetGluLeuCysGluGlyGluLeuPheGlyArg 100
DB 397 GATAACGAGAACGTCGATCTGGTTATGAGCTTTGTGAAGAGAGGTGAGCTTTTGTATCG 456
QY 101 IleValAlaArgGlyHisTyrThrGluArgAlaAlaAlaThrValAlaArgThrIleAla 120
DB 457 ATTGTGTCTAGAGGACATTACAGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 516
QY 121 GluValValArgMetCysHisValAenGlyValMetHisArgAspLeuLysProGluAen 140
DB 517 GAGGTGTGATGATGTCTCACTTAATGAGTTATGATCGAGATTGAAACCTGAGAT 576
QY 141 PheLeuPheAlaAasnLysLysGluAenSerAlaLeuLysAlaIleAspPheGlyLeuSer 160
DB 577 TTCTTGTGTCTAATAAAGAGAGATTCTCCACTAAGGCTATTGATTTGGCTTGTCT 636
QY 161 ValLeuPheLysProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAla 180
DB 637 GTGTTCTTCAAAACCTGAGATAAGTTTACAGAGATTGTAGGAAGTCCGCTATTATATGCT 696
QY 181 ProGluValLeuLysArgAenTyrGlyProGluValAspValTyrSerAlaGlyValIle 200
DB 697 CCAGAAGTGTGAAGAGAGATTATGACAGGGTGTGTGTGAGTCCCGGAGTTAT 756
QY 201 LeuTyrIleLeuLysCysGlyValProPheThrAlaGluThrGluGlnGlyValAla 220
DB 757 ATCTATATCTTGTCTGTGTCTCTCGTCTTGGGCTGAGACTGAACAGGTGTGCT 816
QY 221 LeuAlaIleLeuArgGlyValLeuAspPheLysArgAspProTyrSerGlnIleSerGlu 240
DB 817 CTTCGATCTTCCGGGAGTCTTGTGAAGCAGATGTTGGATCCTGATCCGACTAAGCGGTNACTGCT 876
QY 241 SerAlaLysSerLeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAla 260
DB 877 AGTGCAAGAGCTTGTGAAGCAGATGTTGGATCCTGATCCGACTAAGCGGTNACTGCT 936
QY 261 GlnGlnValLeuAspHisProTyrIleGlnAenAlaLysLys 274
DB 937 CAGCAAGTGTAGCTCACCCATGGATACAGAAATGCAAGAAA 978

RESULT 4

US-10-424-599-37843
; Sequence 37843, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 37843
; LENGTH: 2628
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_134173C.1

US-10-424-599-37843

Alignment Scores:

Pred. No.: 5.1e-147 Length: 2628
Score: 1252.00 Matches: 236
Percent Similarity: 92.34% Conservative: 17
Best Local Similarity: 86.13% Mismatches: 21
Query Match: 88.23% Indels: 0
DB: 18 Gaps: 0

US-08-989-881-2 (1-274) x US-10-424-599-37843 (1-2628)

```
Qy 1 MetAlaAsnGlnThrGlnIleSerAspLysThrIleLeuGlyArgGluLeuGlyArgGly 20
Db 194 GTGACGTACGAGCGGAGCTCATCGGCAAGTACGTGATAGCCGGGAGCTAGGTCTGGGC 253
Qy 21 GluPheGlyIleThrTyrLeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLys 40
Db 254 GAGTTCGGGATAACGTACCTCTGACGAGCCGCGAAGCAAGAGCAGGAGCTCGGTGCAAG 313
Qy 41 SerIleSerLysArgLysLeuArgThrAlaValAspValGluAspValArgGluVal 60
Db 314 TCGATCTCGAAGCGGAGAGCTGAGAACCGGATCGACGTGGAGGACGTGCGCGAGAGGTG 373
Qy 61 ThrIleMetSerThrLeuProGluHisProAsnValValLysLeuLysAlaThrTyrGlu 80
Db 374 CGCATCATGTGACGCTCGCGGAGCAGCGTAACTGTTGAGCTGAAGGCGACTTACGAG 433
Qy 81 AspAsnGluThrValHisLeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArg 100
Db 434 GACGAAGAGAACGTTTCATCTCGTTATGGAGCTTTGCGCGCGGGAGCTCTTTGATCGG 493
Qy 101 IleValAlaArgGlyHisTyrThrGluArgAlaAlaThrValAlaArgThrIleAla 120
Db 494 ATCTCGCGGGGGGCACTACAGCGAGCGTGGCGCGCGAAGCTGGGGAGGACTATTGCT 553
Qy 121 GluValValArgMetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAsn 140
Db 554 GAGTGTGTAGATGTGTACGCCCAATGGTGTATGATCATCGACCTTAAGCCAGAGAA 613
Qy 141 PheLeuPheAlaAsnLysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSer 160
Db 614 TTTCTCTTTTGGAAATAAGAGGAGAAATTCGTCTCAAGGCTATTGACTTTGGTCTCTGT 673
Qy 161 ValLeuPheLysProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAla 180
Db 674 GTGTTTTTCATTCAGGGGAGAGTTTGTGAGATTGTTGGAGTCTCTTACTACATGCGG 733
Qy 181 ProGluValLeuLysArgAsnTyrGlyProGluValAspValTyrSerAlaGlyValIle 200
Db 734 CCGGAGGTTTGAACCGGAATATGGGCCAGAGGTTGATGTGGAGTGTGGGGTGATT 793
Qy 201 LeuTyrIleLeuLeuCysGlyValProPheThrAlaGluThrGluGlnGlyValAla 220
Db 794 CTTTATATTGTTGTGGTGTCTCCGTTTGGGCGAGGCGGAGGCGGAGGCGGTGGCT 853
Qy 221 LeuAlaIleLeuArgGlyValLeuAspPheLysArgAspProTyrSerGlnIleSerGlu 240
Db 854 TTGGCGATCTTGAGGTGTGATTGACTTCAAGAGGGAACCTTGGCCACAGATATCGGAG 913
Qy 241 SerAlaLysSerLeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAla 260
Db 914 AGTGCCAGAGCTTGTGGCGGAAATGTTGGAGCCGATCCTAAAAAGCCCTTGACAGCG 973
Qy 261 GlnGlnValLeuAspHisProTyrIleGlnAsnAlaLysLys 274
Db 974 GAACAGGTGCTTGAACATCCCTGCTACAAAATGCAAGAAA 1015
```

RESULT 5

US-10-425-114-10952

; Sequence 10952, Application US/10425114

; Publication No. US2004003488A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E.

; APPLICANT: Tabaska, Jack E.

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(5313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 10952

; TYPE: DNA

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: 700989873_FLI

US-10-425-114-10952

Alignment Scores:

Pred. No.: 1.68e-146 Length: 1787
Score: 1246.00 Matches: 235
Percent Similarity: 92.70% Conservative: 19
Best Local Similarity: 85.77% Mismatches: 20
Query Match: 87.81% Indels: 0
DB: 18 Gaps: 0

US-08-989-881-2 (1-274) x US-10-425-114-10952 (1-1787)

```
Qy 1 MetAlaAsnGlnThrGlnIleSerAspLysThrIleLeuGlyArgGluLeuGlyArgGly 20
Db 187 GTACGTCACGAGCGCTCATCGGCAAGTACGTGATAGCCGGGAGCTAGGTCTGGTC 246
Qy 21 GluPheGlyIleThrTyrLeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLys 40
Db 247 GAGTTCGGGATAACGTACCTCTGCACGAGCCGCGAAGCAAGCAGGAGCTCGGTGCAAG 306
Qy 41 SerIleSerLysArgLysLeuArgThrAlaValAspValGluAspValArgGluVal 60
Db 307 TCGATCTCGAAGCGGAGCTGAGAACCGCATCGACGTGGAGGACGTGGCGGAGAGGTG 366
Qy 61 ThrIleMetSerThrLeuProGluHisProAsnValValLysLeuLysAlaThrTyrGlu 80
Db 367 CGCATCATGTGACGCTGCGGAGGACGCTTAAGCTGTGAAGCTGAAGGCGACTTACGAG 426
Qy 81 AspAsnGluThrValHisLeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArg 100
Db 427 GACGAAGAGAACGTTTCATCTCGTTATGGAGCTCTGCGCGCGGGAGGCTCTTTCGACCGG 486
Qy 101 IleValAlaArgGlyHisTyrThrGluArgAlaAlaAlaThrValAlaArgThrIleAla 120
Db 487 ATCGTCGCGCGGGGCACTACAGCGAGCGTGGCGCGCGAAGCTGGCGAGGACCATGTCT 546
Qy 121 GluValValArgMetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAsn 140
Db 547 GAGTTGTTAGGATGTGTACGCCAATGTGTATCATCGACGACCTTAAACCTGAGAA 606
Qy 141 PheLeuPheAlaAsnLysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSer 160
Db 607 TTTCTCTTTCGGAATAAAGAGGAGAAATTCGTCTCAAGGCTATTGACTTTGACTCTCC 666
Qy 161 ValLeuPheLysProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAla 180
Db 667 GTGTTTTTCAAGCCAGGAGGAGGTTTTCGAGAGATTGTGGGAGTCTCTTACTACATGGCG 726
Qy 181 ProGluValLeuLysArgAsnTyrGlyProGluValAspValTyrSerAlaGlyValIle 200
Db 727 CCGGAGGTATTGAAAGAGAAATTTATCGGCCAGAGGTGGATGTGTGGAGTGTCTGGGGT 786
Qy 201 LeuTyrIleLeuLeuCysGlyValProPheThrAlaGluThrGluGlnGlyValAla 220
Db 787 CTTTATATTTTGTGTGGAGTTCCTCGGTTTGGGCGAGAGGACGACGAGGGGTGGCT 846
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QY 221 LeuAlaIleuArgGlyValLeuAaspPheLysAtpProTyrSerGlnIleSerGlu 240
Db 847 TTGGCNAATATTGAGGGAGTGATGACTTCAAGAGAAACCGTGGCTCAGATTTTCAGAT 906
QY 241 SerAlaLysSerLeuValLysGlnMetLeuGluProAaspSerThrLysArgLeuThrAla 260
Db 907 AGTGCTAAGAGTCTGTGGCCAGATGTTGGAGCATGATCCTAAGAAGCGCTTGAGCGCT 966

QY 261 GlnGlnValLeuAaspHisProTyrPheGlnAsnAlaLysLys 274

Db 967 GAACAGGTCTTGAGCATTTCTGGTTACAAAATGCAAGAAA 1008

RESULT 6

US-10-424-599-57457/C
; Sequence 57457, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 57457
; LENGTH: 2126
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_22897C.1
US-10-424-599-57457

Alignment Scores:
Pred. No.: 5,02e-136 Length: 2126
Score: 1164.00 Matches: 217
Percent Similarity: 89.9% Conservative: 24
Best Local Similarity: 80.9% Mismatches: 27
Query Match: 82.0% Indels: 0
DB: 18 Gaps: 0

US-08-989-881-2 (1-274) x US-10-424-599-57457 (1-2126)

QY 7 IleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGlyGluPheGlyIleThrTyr 26
Db 1694 ATCGAGGACCGGTACTCTGTGACCGCGAGCTCGGCGCGCGAGTTGGCGTGCATC 1635
QY 27 LeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLeuSerIleSerLysArgLys 46
Db 1634 CTCCTGCATCGACCGCGACACCGCGAGCTGCTCGCGTGTAAAGAGCATCTCGAAGAGGAAG 1575
QY 47 LeuArgThrAlaValAaspValGluAaspValArgGluValThrIleMetSerThrLeu 66
Db 1574 CTCGGGACGCGTGGAGCTGAGACGCTGCGCGCGAGTCCCATCATATGCGCCACCTG 1515
QY 67 ProGluHisProAsnValValLysLeuLysAlaThrTyrGluAaspAsnGluThrValHis 86
Db 1514 CCGGAGAGCCCGAGCATGCTGTGCTCGCGCGAGCTGTGAGGACGACAAATGCCCTCCAC 1455
QY 87 LeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArgIleValAlaArgGlyHis 106
Db 1454 CTCGTGATGGAGCTCTGGAGGGCGGGAACCTTCGAGCGGATCGTCCCGCGGGGAC 1395
QY 107 TyrThrGluArgAlaAlaThrValAlaArgThrIleAlaGluValValArgMetCys 126
Db 1394 TACACGAGCGCGCGCGCGCGCTACCGCGAGCATGCTGAGGTCTGTCAGCTCTGC 1335
QY 127 HisValAenGlyValMetHisArgAspLeuLysProGluAaspPheLeuPheAlaAsnLys 146
Db 1334 CACAAGCAGCGGGTTCATCCACCGAGACCTCAAGCCGAGAACTTCTTGTTCGCAACAAG 1275

QY 147 LysGluAenSerAlaLeuLysAlaIleAaspPheGlyLeuSerValLeuPheLysProGly 166
Db 1274 AAGGAGAATTTGCCCTCAAGCTATTGACTTTGGCTCTCCATATTCTTCAAGCCAGGT 1215
QY 167 GluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluValLeuLysArg 186
Db 1214 GAGAGTTCTCAGAAATTTGTTGGAAGTCCATATTATATGGCTCCAGAGTGTCTCAAGCGG 1155
QY 187 AsnTyrGlyProGluValAaspValTrpSerAlaGlyValIleLeuTyrIleLeuLeuCys 206
Db 1154 AATTATGGACCAGAAATAGATATATGGAGTGCAGGAGTAATTTCTCTACATCTTATTGTGT 1095
QY 207 GlyValProProPheTrpAlaGluThrGluGlnGlyValAlaLeuAlaIleLeuArgGly 226
Db 1094 GTGTTCCTCCCATTTGGCTGAAATCTGAGCAAGAGTTGCACAGCCCATTTCTTCGAGA 1035
QY 227 ValLeuAaspPheLysArgAaspProTyrSerGlnIleSerGluSerAlaLysSerLeuVal 246
Db 1034 CTTATAGATTTTAAAGGGAACCATGGCCAGTATTTCTGAAAGTGTCTAAAGCCCTTGT 975
QY 247 LysGlnMetLeuGluProAaspSerThrLysArgLeuThrAlaGlnValLeuAaspHis 266
Db 974 AGGCAATGTTAGAACCAAGCCCAAGCTTCGATTAACCTGCCAAACAAGTGTCTGAGCAT 915
QY 267 ProTyrPheGlnAsnAlaLysLys 274
Db 914 CCTGGATTCAAAATGCTAAGAAG 891

RESULT 7

US-10-437-963-7404
; Sequence 7404, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 7404
; LENGTH: 1978
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_14001C.1
US-10-437-963-7404

Alignment Scores:
Pred. No.: 6.21e-135 Length: 1978
Score: 1155.00 Matches: 216
Percent Similarity: 88.81% Conservative: 22
Best Local Similarity: 80.60% Mismatches: 30
Query Match: 81.40% Indels: 0
DB: 19 Gaps: 0

US-08-989-881-2 (1-274) x US-10-437-963-7404 (1-1978)

QY 7 IleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGlyGluPheGlyIleThrTyr 26
Db 234 ATCGCGCGCGGTACGAGCTGGGCGGAGTCTCGGCGCGGAGTTCGGGTTCACCTAC 293
QY 27 LeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerLysArgLys 46
Db 294 CTCCTCAGCGGAGCGGAGCGGCGGCGCTTACGCTGCAAGTCCATCTCCAAGAAGAAG 353

47	LeuArgThrAlaValAspValGluAspValArgArgGluValThrIleMetSerThrLeu	66
354	CTCCGACCCGCGTGGACATCGAGAGCGTCCGCGGAGGTGGACATCATCGCCACCTC	413
67	ProGluHisProAsnValValLeuLeuLeuAlaThrTyrGluAspAsnGluThrValHis	86
414	CCCAAGCACCCCAACATCGTCACGCTCCGGGACACCTACGAGGACGACAATGCCGTCAC	473
87	LeuValMetGluLeuLeuCysGluGlyGlyGluLeuPheGlyArgIleValAlaArgGlyHis	106
474	CTCGTCATGAGGCTCTCGAGGGCGGGAGCTCTTCGACCGGATCGTCGCGCGGGGCGCAC	533
107	TyrThrGluArgAlaAlaAlaThrValAlaArgThrIleAlaGluValValArgMetCys	126
534	TACACCGAGCGCGCGCGCGCTGCTCACCGCACCATCGTCGAGGTCGTGCAGATGTGC	593
127	HisValAsnGlyValMetHisArgAspLeuLeuProGluAsnPheLeuPheAlaAsnLys	146
594	CATAAGCATGGAGTGATGCACCGGGACCTCAACACAGAGAATTTCTTTGTGCAACAACAG	653
147	LysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysProGly	166
654	AAGGAACTCGAGCTCTGAAGGCAATTTGATTTGGCCTGCTGTTTTTTCACCCCAAGGT	713
167	GluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluValLeuLysArg	186
714	GAACGGTTCACTGAGATTGTCGGAAGCCCTATTATACATGGCTCCTGAGGTGCTAAAGAGA	773
187	AsnTyrGlyProGluValAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeuCys	206
774	AAATTATGGCCCTGAGGTGTGATGTTTGAGGTGCAGGAGTGATCCTTTTACATCTCTCTTGT	833
207	GlyValProPheTrpAlaGluThrGluGlnGlyValAlaLeuAlaIleLeuArgGly	226
834	GGAGTCCCTCCATTTTGGCGAGAACTGAACAGGGTGTGCTCAGGCAATATCCGTTCT	893
227	ValLeuAspPheLysArgAspProTrpTrpSerGlnIleSerGluSerAlaLysSerLeuVal	246
894	GTCATTCACTTCAAGAGAGACCCCATGGCCAAAGGGTCTCAGATATGCAAAAGGATCTTGTC	953
247	LysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGlnValLeuLeuAspHis	266
954	AAGGGAATGCTCAATCCAGACCCCTAGCGCGCGGCTAAATGCTCAACAGGTGCTTGATCAT	1013
267	ProTrpIleGlnAsnAlaLysLys	274
1014	CTTTGGTTACAGACATTAAAGAAG	1037

RESULT 8

US-10-425-114-34236
Sequence 34236, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53113)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128

Alignment Scores:	7.18e-134	Length:	2149
Pred. No.:	1147.00	Matches:	215
Score:	89.18%	Conservative:	24
Percent Similarity:	80.22%	Mismatches:	29
Best Local Similarity:	80.83%	Indels:	0
Query Match:	18	Gaps:	0
DB:			
US-08-989-881-2 (1-274) x US-10-425-114-34236 (1-2149)			
Qy	7	IleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGlyGluPheGlyIleThrTyr	26
Db	458	ATCGCGCGGTACGAGCTCGCGCGGAGCTCGGCGCGGAGTTCGGGGTTACCTAC	517
Qy	27	LeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerLysArgLys	46
Db	518	CTCTGCACACACCGCGCTCAGGGGAGGGCGCTGCCCTGCAAGTCCATCTCCAAGAAGAAG	577
Qy	47	LeuArgThrAlaValAspValGluAspValArgArgGluValThrIleMetSerThrLeu	66
Db	578	CTCCGACCGCGCTCGACCTCGAGGACGTGCGCGGGAGGTCCAGATCATGCCCACTC	637
Qy	67	ProGluHisProAsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrValHis	86
Db	638	CCCAAGCACCCCAACGTCGTACGCTCAGGGACACGTACGAGGACGACAAATCGCGTGCAC	697
Qy	87	LeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArgIleValAlaArgGlyHis	106
Db	698	CTCGTCATGAGCTCTCGAGGCGGTGAGCTCTTCGACCGCATCGTCGCGCGGGACAC	757
Qy	107	TyrThrGluArgAlaAlaThrValAlaArgThrIleAlaGluValValArgMetCys	126
Db	758	TACACTGAGCGTCTCCCGCTTGGTCTTACGCATATTGTTGAGTCTGTCAGATGTGC	817
Qy	127	HisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsnLys	146
Db	818	CATAAGCATGGAGTGATGCACAGGATCTCAACACAGAAAAATTCITGTTGCAACAAG	877
Qy	147	LysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysProGly	166
Db	878	AAAGAAATCAGCGGCACCTTAAGGCATTTGATTTTGGCTCTCTGTATTTTTCACACAGGC	937
Qy	167	GluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluValLeuLysArg	186
Db	938	GAACGGTTTCTCAGATTGTTGGAAGTCTTATTACATGGCTCCAGAGGTGCTTAAGAGA	997
Qy	187	AsnTyrGlyProGluValAspValTrpSerAlaGlyValIleLeuTyrIleLeuLysCys	206
Db	998	AACTATGGCCACAGGTTGATGTTTGGAGTGCAGGAGTGATCTGTATCTCTCTTTGT	1057
Qy	207	GlyValProProPheTrpAlaGluThrGluGlnGlyValAlaLeuAlaIleLeuArgGly	226
Db	1058	GGTGTCCCCCATTCCTGGCGAGAAACGGAACAGGGTGTGGCTCAGGCAATCATTCGATCT	1117
Qy	227	ValLeuAspPheLysArgAspProTrpSerGlnIleSerGluSerAlaLysSerLeuVal	246
Db	1118	GTCAITGATTTCAAAAGATCCATGGCCACAGGGTGTCTGTATAACGCCCAAGACCTTGT	1177
Qy	247	LysGluMetLeuGluProAspSerThrLysArgLeuThrAlaGlnGlnValLeuAspHis	266
Db	1178	AGAGAAATGCTGAATCCGGACCCCAAAACACGAGTTCACAGCTCACCAAGTGTGTGTGCAC	1237
Qy	267	ProTrpIleGlnAsnAlaLysLys	274
Db	1238	CCATGTTGTCAGAACATTAAAGAG	1261

RESULT 9

US-10-425-114-28411
; Sequence 28411, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong

```
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 28411
; LENGTH: 2244
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4757-010-H10_FLI
US-10-425-114-28411

Alignment Scores:
Pred. No.: 2,45e-133 Length: 2244
Score: 1143.00 Matches: 215
Percent Similarity: 88.81% Conservativeness: 23
Best Local Similarity: 80.22% Mismatches: 30
Query Match: 80.55% Indels: 0
DB: 18 Gaps: 0

US-08-989-881-2 (1-274) x US-10-425-114-28411 (1-2244)
Qy 7 IleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGluPheGlyIleThrTyr 26
Db 541 ATCGCGCGCGGTACGAGCTCGCGCGGAGCTCGCGCGGAGTTCGGGGTTACCTAC 600
Qy 27 LeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerIleArgLys 46
Db 601 CTCTGCACAGACCGGTCTCGAGGCGGCGGTGCGCTGCAAGTCTATCTCCAAGAAGAAG 660
Qy 47 LeuArgThrAlaValAspValGluAspValArgGluValThrIleMetSerThrLeu 66
Db 661 CTCGACACCGCGTCTCGAGGAGTTCGCGCGGAGTTCGAGATCATGCGCCACCTC 720
Qy 67 ProGluHisProAsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrValHis 86
Db 721 CCCAAGCACCCCAAGTCTGTCAGCTCAGGACGAGTTCAGGACGACCAATGCCGTGCAC 780
Qy 87 LeuValMetGluLeuCysGluGlyGluLeuPheGlyArgIleValAlaArgGlyHis 106
Db 781 CTCGTATGAGAGTCTCGAGGCGGTGAGTCTTTCGACCGCATCGTGGCGCGGGGACAC 840
Qy 107 TyrThrGluArgAlaAlaThrValAlaArgThrIleAlaGluValValArgMetCys 126
Db 841 TACACTGAGCGTCTGCGCGCTTGTGCTTACGCACTATCGTGTGAGTCTGTCGAGATGTC 900
Qy 127 HisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsnLys 146
Db 901 CATAAGCATGAGTATGCACAGGATCTCAACACCAAGAAATTTTGTGTTGCAACCAAG 960
Qy 147 LysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysProGly 166
Db 961 AAAGAAATCAGCGGCACCTTAAGGCCATTTGATTTGGCCTGTCTGTATTTTCACTCCAGGC 1020
Qy 167 GluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluValLeuLysArg 186
Db 1021 GAACGGTTTCTGAGATTGTTGGAAGTCTTATTACATGGCTTCAGAGGTCTAAAGAGA 1080
Qy 187 AsnTyrGlyProGluValAspValTrpSerAlaGlyValIleLeuTyrIleLeuLysCys 206
Db 1081 AACTATGCCCCAGAGTTGATGTTGGAGTGCAGAGTGATTCGTACATCTCTCTTTGT 1140
Qy 207 GlyValProProPheThrAlaGluThrGluGlnGlyValAlaLeuAlaIleLeuArgGly 226
Db 1141 GGTGTCCTCCCATTTCTGGGCAGAAACGGAACAGGGTGTGTCTCAGGCAATCATTCGATCT 1200
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Qy 227 ValLeuAspPheLysArgAspProTrpSerGlnIleSerGluSerAlaLysSerLeuVal 246
Db 1201 GTCAATTGATTTCAAAAGAGATCCATGGCCAAAGGTGTCTGATAACGCCAAAGACCTTGTTC 1260
Qy 247 LysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGlnGlnValLeuAspHis 266
Db 1261 AGAGGAATGCTGAATCCGGACCCCAAAACGACGATTGACAGCTCACCNAAGTCTTGGTCAC 1320
Qy 267 ProTrpIleGlnAsnAlaLysLys 274
Db 1321 CCATGGTTGCAGAACATTAGAAG 1344

RESULT 10
US-10-425-115-28928
; Sequence 28928, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 28928
; LENGTH: 2298
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_126393C.1
US-10-425-115-28928

Alignment Scores:
Pred. No.: 2,54e-133 Length: 2298
Score: 1143.00 Matches: 215
Percent Similarity: 88.81% Conservativeness: 23
Best Local Similarity: 80.22% Mismatches: 30
Query Match: 80.55% Indels: 0
DB: 20 Gaps: 0

US-08-989-881-2 (1-274) x US-10-425-115-28928 (1-2298)
Qy 7 IleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGluPheGlyIleThrTyr 26
Db 546 ATCGCGCGCGGTACGAGCTCGCGCGGAGTTCGGCGCGGAGTTCGGGGTTACCTAC 605
Qy 27 LeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerIleArgLys 46
Db 606 CTCGTGCACAGACCGCGCTCAGGGGAGGCGCTGCGCTGCAAGTCCATCTCCAAGAAGAAG 665
Qy 47 LeuArgThrAlaValAspValGluAspValArgGluValThrIleMetSerThrLeu 66
Db 666 CTCGACACCGCGTCTCGACCTCGAGGACGTGCGCGCGGAGTTCGAGATCATGCGCCACCTC 725
Qy 67 ProGluHisProAsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrValHis 86
Db 726 CCCAAGCACCCCAAGTCTGTCAGGACGAGTTCAGGACGACCAATGCCGTGCGTGCAC 785
Qy 87 LeuValMetGluLeuCysGluGlyGluLeuPheGlyArgIleValAlaArgGlyHis 106
Db 786 CTCGTATGAGAGTCTCGAGGCGGTGAGTCTTTCAGCGCATCTGTCGCGCGGGGACAC 845
Qy 107 TyrThrGluArgAlaAlaThrValAlaArgThrIleAlaGluValValArgMetCys 126
Db 846 TACACTGAGCGTCTGCGCGCTTGTGCTTACGCACTATCGTGTGAGTCTGTCGAGATGTC 905
Qy 127 HisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsnLys 146
Db 906 CATAAGCATGAGTATGTCACAGGATCTCAACACCAAGAAATTTTCTTGTGTTGCAACCAAG 965
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Score:	1136.00	Matches:	212
Percent Similarity:	88.81%	Conservative:	26
Best Local Similarity:	79.10%	Mismatches:	30
Query Match:	80.06%	Indels:	0
DB:	18	Gaps:	0

US-08-989-881-2 (1-274) x US-10-425-114-33866 (1-2076)

Qy	7	IleSerAspLysTyrIleLeuGlyArgGluIleuGlyArgGlyGluPheGlyIleThrTyr	26
Db	337	ATCAGCACAAAGTAGTCTCGGACAGGAGAGTTCGGCCGGGGAGTTCTGGGTACAGTAC	396
Qy	27	LeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerLysArgLys	46
Db	397	CTGTGTATGGATCGGGACACCAAGAGAGTCTCGCTCTGCAAGTCCATCTCCAAGCGCAAG	456
Qy	47	LeuArgThrAlaValAspValAlaAspValArgArgGluValThrIleMetSerThrLeu	66
Db	457	CTCGGACGGCCGTCAGCTGGAGGACGTGCGCGGAGGTGGCCATCATGCGCCACCTG	516
Qy	67	ProGluHisProAsnValValLeuLysAlaThrTyrGluAspAsnGluThrValHis	86
Db	517	CCCAAGAGCCCGAGCTGTCTCTCGCGGGAGCGTCGAGGACGACGGCGCGCTCCAC	576
Qy	87	LeuValMetGluLeuCysGluGlyGluLeuPheGlyArgIleValAlaArgGlyHis	106
Db	577	CTCGTCATGGAGCTCTCGAGGGCGGCGAGCTCTTCGACCGCATCGTCGCGGGGECAC	636
Qy	107	TyrThrGluArgAlaAlaThrValAlaArgThrIleAlaGluValValArgMetCys	126
Db	637	TACACGAGCGCGCGCGCAGTGTACCGCGCACCATCTCTGAGGTCTCGAGTCTGCTGC	696
Qy	127	HisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsnLys	146
Db	697	CACCGCACGGCGTCAATCCACCGGACCTCAAGCGGAGAACTTCTCTTCGCCAATAAG	756
Qy	147	LysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysProGly	166
Db	757	AAGGAGAACTCGCCGCTCAAGGCCATCGACTTCGGTCTCTCCATCTTCTCAAGCCTGCT	816
Qy	167	GluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluValLeuLysArg	186
Db	817	GAAAGATTTTCAGAAATTTGCGGAAGCCCTATTACATGGGTCTCTGAAGTAGTGAAGA	876
Qy	187	AsnTyrGlyProGluValAspValTyrSerAlaGlyValIleLeuTyrIleLeuLeuCys	206
Db	877	AACTATGGCGCAGAAATAGACATATGAGTCTCGGAGTTATCTGTATATTATTATGT	936
Qy	207	GlyValProProPheThrAlaGluThrGluGlnGlyValAlaLeuAlaIleLeuArgGly	226
Db	937	GGAGTCTCTCCATTTTGGCTTGAGACTGAACAAGGGGTGGCGCAGGCTATTCTTCGTGA	996
Qy	227	ValLeuAspPheLysArgAspProTrpSerGlnIleSerGluSerAlaLysSerLeuVal	246
Db	997	AATATCGATTTTAAGCGGGAACCTCTGGCCCTAATGTTCGAAAAATGCAAAAGATTAGTT	1056
Qy	247	LysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGlnGlnValLeuAspHis	266
Db	1057	CGACACATGTTGGAGCCTGATCCAAAGCTCAGGCTACTGTCAAAGCAGGTTCTTGAACAT	1116
Qy	267	ProTrpIleGlnAsnAlaLysLys	274
Db	1117	CATTGGCTTCAAAATGCAAGAAG	1140

RESULT 13

US2004021425115
US-10-425-115-13710
; Sequence 13710, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

```
Db 1089 CGACATGTTGGAGCCTGATCCAAAGCTCAGGCTAACTGCAAGCAGGTTCTTGAACAT 1148
Qy 267 ProTrpIleGlnAsnAlaLysLys 274
Db 1149 CATTGGCTTCAAAATGCAAGAG 1172

RESULT 14
US-10-767-701-13220
; Sequence 13220, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(5335)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 13220
; LENGTH: 1388
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS5983_1
US-10-767-701-13220

Alignment Scores:
Pred No.: 1,26e-132 Length: 1388
Score: 1135.00 Matches: 211
Percent Similarity: 88.43% Conservative: 26
Best Local Similarity: 78.73% Mismatches: 31
Query Match: 79.99% Indels: 0
DB: 19 Gaps: 0

US-08-989-881-2 (1-274) x US-10-767-701-13220 (1-1388)
Qy 7 IleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGlyGluPheGlyIleThrTyr 26
Db 312 ATCCAGCACAAGTAGTCTGCTCGACAGGAGCTCGGCCGCGGAGTTCGGGGTGCAGCTAC 371
Qy 27 LeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerIleArgLys 46
Db 372 CTGTGCATGATCGGAGCACCAGAGAGCTGCTCGCTGCAAGTCCATCTCCAAGCGCAAG 431
Qy 47 LeuArgThrAlaValAspValArgGluValArgGluValThrIleMetSerThrLeu 66
Db 432 CTGGGACGGCGCTCGAGCTCGAGGACCTGCGCGGAGGTGGCCATCATGCCACCTA 491
Qy 67 ProGluHisProAsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrValHis 86
Db 492 CCCAAGAGCCCGCAGCATCTGTCTCGCGGAGCGTGCAGGACGAGGCGCGCTCCAC 551
Qy 87 LeuValMetGluLeuCysGluGlyGluLeuPheGlyArgGluValAlaArgGlyHis 106
Db 552 CTGTGTCATGAGACTCTGCGAGCGCGGAGCTCTTCGACCGCATCTGCGCGGAGAC 611
Qy 107 TyrThrGluArgAlaAlaAlaThrValAlaArgThrIleAlaGluValValArgMetCys 126
Db 612 TACACCGAGCGCGCGCGCCCAATGTACCCCGCACCATTGTCGAGGTCTGTCAGCTTCG 671
Qy 127 HisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsnLys 146
Db 672 CACCGCCACCGCGTATCCACCGGACCTCAAGCGGAGAACTTCTCTTCGCCAATAAG 731
Qy 147 LysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysProGly 166
Db 732 AAGGAGAACTCGCCCTCAAGCCCATCGACTTCGGCCTCTCCATCTTCTCAAGCTGCT 791
Qy 167 GluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluValLeuLysArg 186
Db 167 GluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluValLeuLysArg 186
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Db 792 GAAAGGTTTTTCAGAAATTTGTTGGGAGCCCTATTACATGGCTCCTGAAGTATTGAAGAGA 851
Qy 187 AsnTyrGlyProGluValAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeuCys 206
Db 852 AACTATGGCCAGAAATAGACATATGAGTGGGAGTTCCTGTATATTTTATTTATGT 911
Qy 207 GlyValProProPheTrpAlaGluThrGluGlnGlyValAlaLeuAlaIleLeuArgGly 226
Db 912 GGAGTTCTCTCATTTTGGGCTGAGACTGAACAAGGGGTGGCAGGCTATTCTTCGTGGA 971
Qy 227 ValLeuAspPheLysArgAspProTrpSerGlnIleSerGluSerAlaLysSerLeuVal 246
Db 972 AATATCGATTTTAAGCGGGAACCTGGCTTAATGTTTCAGAAATGCAAAAGATTAGTT 1031
Qy 247 LysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGlnGlnValLeuAspHis 266
Db 1032 CGACGATGTTGGAGCCTGATCCAAAGCTCAGGTTAACTGCAAGCAGGTTCTTGAACAT 1091
Qy 267 ProTrpIleGlnAsnAlaLysLys 274
Db 1092 CATTGGCTTCAAAATGCAAGAG 1115

RESULT 15
US-10-260-238-574
; Sequence 574, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260,238
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 574
; LENGTH: 1770
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-260-238-574

Alignment Scores:
Pred. No.: 4,28e-132 Length: 1770
Score: 1132.00 Matches: 211
Percent Similarity: 88.06% Conservative: 25
Best Local Similarity: 78.73% Mismatches: 32
Query Match: 79.77% Indels: 0
DB: 17 Gaps: 0

US-08-989-881-2 (1-274) x US-10-260-238-574 (1-1770)
Qy 7 IleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGlyGluPheGlyIleThrTyr 26
Db 217 ATCGACACAAGTAGCTGCGCTGAGCGGAGCTCGGCGGGGAGTTTCGGGGTGCAGCTAC 276
Qy 27 LeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerLysArgLys 46
Db 277 CTGTGTCATGATCGGAGCACCAGAGAGCTGCTCGCTTCCAAAGTCCATCTCCAAAGCGGAG 336
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OY 47 LeuArgThrAlaValAspValGluAspValArgGluValThrIleMetSerThrLeu 66
Db |||||
OY 337 CTGAGAGCGCGGTTCAGCTGGAGGACGTGCGCGGAGGTGCCCATCATGCCACCTC 396
Db |||||
OY 67 ProGluHisProAsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrValHis 86
Db |||||
OY 397 CCCAAGAGCGCCAGCATCGTGTGCTGCGGAGGCGTGCAGGACGAGGCGCGTGCAC 456
Db |||||
OY 87 LeuValMetGluLeuGlyGluGlyGluLeuPheGlyArgIleValAlaArgGlyHis 106
Db |||||
OY 457 CTCGTATGGAGCTCTCGAAGCGGGAGCTCTTCACCGCATCGTCGCGCGGGGCCAC 516
Db |||||
OY 107 TyrThrGluArgAlaAlaThrAlaThrIleAlaGluValValArgMetCys 126
Db |||||
OY 517 TACACGGAGCGCGCCGCCCATGTGACCCGCCCATCGTGAGGTCTGCCAGCTCTGC 576
Db |||||
OY 127 HisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsnLys 146
Db |||||
OY 577 CACCGCCAGCGCGTTATCCACCGGACCTCAAGCCGAGAACTTCCTCTTCGCCAACAG 636
Db |||||
OY 147 LysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysProGly 166
Db |||||
OY 637 AAGGAGAACTCGCGCTCAAGGCCATCGATTCGGGCTCTCCATCTTCTCAAGCCCGGT 696
Db |||||
OY 167 GluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluValLeuLysArg 186
Db |||||
OY 697 GAGAACTTCTGAAATTGTGGAGAGCCCATATTACATGGCTCCAGAGGTATTGAAGAGA 756
Db |||||
OY 187 AsnTyrGlyProGluValAspValTrpSerAlaGlyValIleLeuTyrIleLeuLysCys 206
Db |||||
OY 757 AACTATGGTCCGGAATAGATATTGGAGTGCAGGAGTTATCTGTATATTTTGTATGT 816
Db |||||
OY 207 GlyValProProPheThrAlaGluThrGluGlnGlyValAlaLeuAlaIleLeuArgGly 226
Db |||||
OY 817 GGAGTTCTCCATTTTGGGCTGAGACTGAGCAAGGGGTGGCAAGCCATTCTTCGTGGA 876
Db |||||
OY 227 ValLeuAspPheLysArgAspProTrpSerGlnIleSerAlaLysSerLeuVal 246
Db |||||
OY 877 AATATCGATTTCAACCGGNACCTGCGCAAAATGTTTCAGAAAATGCTAAAGATTGGTT 936
Db |||||
OY 247 LysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGlnGlnValLeuAspHis 266
Db |||||
OY 937 CGACGCATGTTGGAGCTGATCCAAAACCTCAGGTTAACTGCAAAAGCAAGTTCTTGAACAT 996
Db |||||
OY 267 ProTrpIleGlnAsnAlaLysLys 274
Db |||||
OY 997 CCATGGCTTCAAAATGCTAAGAAA 1020
Db |||||
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Search completed: October 14, 2005, 20:55:30
Job time : 773 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 14, 2005, 18:23:22 ; Search time 3512 seconds
(without alignments)
2969.707 Million cell updates/sec

Title: US-08-989-881-2
Perfect score: 1419
Sequence: 1 MANQTQSDKYLRELGRG.....TKRLTAQVLDHPWQNAKK 274

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO_epool/US08989881/runat_14102005_112734_5205/app_query.fasta_1.455
-DB=EST -QFMT=fastap -SUFFI=rat -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USFR=US08989881 @CGN 1_1 4352 @runat_14102005_112734_5205 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEVTIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST.*

1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gest1.*
9: gb_gest2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1141	80.4	1963	CNSOA743	BX822805 Arabidops
2	1132	79.8	1770	CL960178	CL960178 OsIFCC003
3	1116	78.6	2037	CNSA01F3	BX830195 Arabidops
4	1102	77.7	833	BE641223	BE641223 Cr12.2_K0
5	1094	77.1	1964	CNSOA40L	BX824980 Arabidops
6	1046	73.7	1840	CNSOA93C	BX821136 Arabidops
7	1042	73.4	768	BU003544	BU003544 QG35J03
8	1011	71.2	721	CK250764	CK250764 EST734401
9	1005	70.8	711	CA264357	CA264357 SCQGLB204

10	1004	70.8	982	7	CK281626
11	950	66.9	889	7	CK297575
12	945	66.6	864	6	CB894498
13	943	66.5	688	6	CA266323
14	940	66.2	679	5	BQ148394
15	938.5	66.1	914	7	CV470355
16	937	66.0	675	4	BM437749
17	935	65.9	659	2	AW685409
18	931	65.6	961	5	BX839090
19	918	64.7	955	5	CK289074
20	917.5	64.7	649	1	AV941214
21	916	64.6	767	4	BI927392
22	914	64.4	656	2	BF647650
23	912	64.3	642	7	CN897553
24	909	64.1	764	7	CO082724
25	908	64.0	644	6	CA244772
26	907	63.9	778	7	CF394637
27	907	63.9	1719	9	CL969653
28	902	63.6	2110	5	BU103685
29	900	63.4	1233	9	CL978642
30	898	63.3	1647	9	CL967234
31	896	63.1	1737	9	CL963040
32	895	63.1	654	5	BU994538
33	895	63.1	743	5	BQ862699
34	893	62.9	827	6	CB677374
35	890	62.7	681	5	BU001940
36	890	62.7	774	5	BQ802750
37	887	62.5	616	5	BQ859489
38	884	62.3	2566	3	AY109374
39	880	62.0	645	4	BJ226480
40	880	62.0	2298	3	AY109401
41	878	61.9	902	7	CK290574
42	877	61.8	903	7	CK271484
43	876	61.7	957	7	CK255123
44	875	61.7	612	4	BJ479365
45	872.5	61.5	1720	3	CNSOA00T

ALIGNMENTS

RESULT 1
LOCUS CNSOA743 1963 bp mRNA linear HTC 06-FEB-2004
DEFINITION Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTF865ZB09 of Flowers and buds of strain col-0 of Arabidopsis thaliana (thale cress).
ACCESSION BX822805 GI:42466038
VERSION BX822805
KEYWORDS HTC; GSLT cDNA.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE 1 (bases 1 to 1963)
AUTHORS Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissbach, J. and Salanoubat, M.
TITLE Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1963)
AUTHORS Direct Submission
TITLE Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT The sequences are based on single pass reads. Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G. Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,

CK281626	EST744348
CK297575	EST760289
CB894498	EST647290
CA266323	SCAGLB204
BQ148394	NF067H06F
CV470355	43200.1 C
BM437749	VVA024F07
AW685409	NF029A07N
BX839090	BX839090
CK289074	EST751796
AV941214	AV941214
BI927392	EST547281
BF647650	NF077A07E
CN897553	010701AAZ
CO082724	GR_Ea47H
CA244772	SCSFL408
CF394637	RTD82_6 A
CL969653	OsIFCC018
BU103685	SCPRZ100
CL978642	OsIFCC032
CL967234	OsIFCC015
CL963040	OsIFCC008
BU994538	HM07G05T
BQ862699	QGC21M24
CB677374	OSJNE14E
BU001940	OGG2a04_Y
BQ802750	WHE2829_E
BQ859489	QGC13C21
AY109374	Zea mays
BJ226480	BJ226480
AY109401	Zea mays
CK290574	EST753288
CK271484	EST717562
CK255123	EST738760
BJ479365	BJ479365
BX830884	Arabidops


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||||| 909 AACATGCTCTGAGATCGATGTGGAGCGCTGGAGTTATCTCTATATCTCTATTGT 968
||||| 207 GlyValProPheTTPAlaGluThrGluGlnGlyValAlaLeuAlaLeuArgGly 226
||||| 969 GGTGTCGCCCATTTGGCGAGACATGAGCAGGGTGGCTCAAGCATATTAGATCA 1028
||||| 227 ValLeuAspPheLysArgAspProTTPSerGlnIleSerGluSerAlaLysSerLeuVal 246
||||| 1029 GTTATTGACTTTAAAGAGATCCATGCCAAGAGTTTGTGACAGCGCCAAAGACCTTGTG 1088
||||| 247 LysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGlnGlnValLeuAspHis 266
||||| 1089 AGAAGATGCGGTGAACCTGATCCCGAAGAAACGGCTTACTGCTGCACAAAGTTCTCGAACAT 1148
||||| 267 ProTTPileGlnAsnAlaLysLys 274
||||| 1149 ACTGGATAGTGAATGCANAGAG 1172

RESULT 4
BE641223 833 bp mRNA linear EST 01-SEP-2000
LOCUS Ceratopteris Spore Library Ceratopteris richardii
DEFINITION cDNA_clone_Cri2_2_K07_5', mRNA sequence..
ACCESSION BE641223
VERSION BE641223.1 GI:9958885
KEYWORDS EST.
SOURCE Ceratopteris richardii
ORGANISM Ceratopteris richardii
REFERENCE 1 (bases 1 to 833)
AUTHORS Chatterjee,A., San Miguel,P., Stout,S.C., Banks,J. and Roux,S.J.
TITLE Expressed sequence tags of cDNA clones from a C. richardii library
JOURNAL Unpublished (2000)
COMMENT Contact: Roux SJ
Section of Molecular Cell and Developmental Biology
University of Texas
Biology Building, Room 16, Austin, TX 78712, USA
Tel: 512 471 4238
Fax: 512 232 3402
Email: sroux@uts.cc.utexas.edu
Plate: Cri2_2 row: K column: 07
Seq primer: SP6.
Location/Qualifiers
1..833
/organism="Ceratopteris richardii"
/mol_type="mRNA"
/cultivar="Brog"
/db_xref="taxon:49495"
/clone="Cri2_2_K07"
/tissue_type="Gametophyte"
/cell_type="Spore"
/dev_stage="20 hours after germination initiation"
/clone_lib="Ceratopteris Spore Library"
/note="vector: pCMVSPORT6; EST sequence from cDNA library.
cDNA library constructed from mRNA isolated from C.
richardii spores that had developed for 20 hours after
their germination had been initiated by white light."

ORIGIN
Alignment Scores: 2.92e-120 Length: 833
Pred. No.: 1102.00 Matches: 206
Score: 88.08% Conservative: 23
Percent Similarity: 79.23% Mismatches: 31
Best Local Similarity: 77.66% Indels: 0
Query Match: 2 Gaps: 0
DB:

US-08-989-881-2 (1-274) x BE641223 (1-833)

QY 15 ArgGluLeuGlyArgGlyGluPheGlyLeuThrTyrLeuCysThrAspArgGluThrArg 34

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::: 6 AAGAGACTTGGTGGTGAATTTGGCATCCTTACTTATGCAGATCGGAGACTGAC 65
||||| 35 GluAlaLeuAlaCysLysSerIleSerLysArgLysLeuArgThrAlaValAspValGlu 54
||||| 66 GAAGTCTAGCATGTAATCTATTCTTAAGGGAAGCTTAGGACACCCATGACATTGAA 125
||||| 55 AspValArgArgGluValThrIleMetSerThrLeuProGluHisProAsnValValLys 74
||||| 126 GATGTTTGAAGAGAGGTGGATATTATGAGACATCTTCTTAACATCCAAACATCTGTGACT 185
||||| 75 LeuLysAlaThrTyrGluAspAsnGluThrValHisLeuValMetGluLeuCysGluGly 94
||||| 186 TTGAAGGGGTGATGAGGATGAGATGCAGTGCATCTTGTTCATGGAACCTATGTGAAGGT 245
||||| 95 GlyGluLeuPheGlyArgIleValAlaArgGlyHisTyrThrGluArgAlaAlaAlaThr 114
||||| 246 GGTGAATTTGTCATCGCATTTGTAGCAAGAGGTCACTACAGCGAGAGAGCTGCAGCTGCG 305
||||| 115 ValAlaArgThrIleAlaGluValValArgMetCysHisValAsnGlyValMetHisArg 134
||||| 306 GTCATGCGTACCATTTCTTGAAGTTGTACAGTTTGGCATAGGCATGGTGTTCATGCACGCG 365
||||| 135 AspLeuLysProGluAsnPheLeuPheAlaAsnLysLysGluAsnSerAlaLeuLysAla 154
||||| 366 GACCTTAAGCCAGAAAATTTCTGTTTGCANAGAAAGAAAATTCGCCCTTAAAGGCT 425
||||| 155 IleAspPheGlyLeuSerValLeuPheLysProGlyGluArgPheThrGluIleValGly 174
||||| 426 ATTGATTTTGATTTCCATCTTCTTCAAACTTGGGAGAAGTTTACCGAAATAGTAGGA 485
||||| 175 SerProTyrTyrMetAlaProGluValLeuLysArgAsnTyrGlyProGluValAspVal 194
||||| 486 AGTCCATACCTATATGACCTGAGGTACTGAAAAGAAGTTATGGCCAGAGTTGATATA 545
||||| 195 TrpSerAlaGlyValIleLeuTyrIleLeuLysCysGlyValProPheThrAlaGlu 214
||||| 546 TGGAGTGCAGAGTTATCTTTACATCTTTTATGCGGAGTCCCCCTTTTGGGCTGAG 605
||||| 215 ThrGluGlnGlyValAlaLeuAlaIleLeuArgGlyValLeuAspPheLysArgAspPro 234
||||| 606 ACCGAACAAATTAGTAGCCAGGCCATCTTACGTGGAAATGTGGACTTCAACAGAGATCCT 665
||||| 235 TrpSerGlnIleSerGluSerAlaLysSerLeuValLysGlnMetLeuGluProAspSer 254
||||| 666 TGCCCAAAATGTTTCAGAAAATGCTAAAGCGCTAGTCGCGCAAAATGCTTGGACCCAGATCCA 725
||||| 255 ThrLysArgLeuThrAlaGlnGlnValLeuAspPheProTTPileGlnAsnAlaLysLys 274
||||| 726 AGCCAAAGATTGACAGCTCAACAAAGTCTTGATCATCTTGGTGGCTTGTGTAATGCAAGAAA 785

CNS0A4QL 1964 bp mRNA linear HTC 06-FEB-2004
Arabidopsis thaliana Full-length cDNA Complete sequence from clone
GSLTGH872B07 of Hormone Treated Callus of strain col-0 of
Arabidopsis thaliana (thale cress).
BX824980
BX824980.1 GI:42462449
HTC; GSLT cDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopses.
1 (bases 1 to 1964)
Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,
Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
Whole Genome Comparisons and 'Full-length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
Annotation
Unpublished
JOURNAL

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/tissue_type="Silique"
/plasmid="pCMVSPORT_6"
complement(1..1840)
/gene="At2g41860"

ORIGIN
Alignment Scores:
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Pred. No.:      Matches: 193
Score:          1046.00
Percent Similarity: 85.87%   Conservative: 38
Best Local Similarity: 71.75% Mismatches: 37
Query Match:     73.71%     Indels: 1
DB:              3          Gaps: 0

US-08-989-881-2 (1-274) x CNS0A93C (1-1840)

Qy      6 GlnileSerAspLysTyrIleLeuGluValArgGluLeuGlyArgGlyGluPheGlyIleThr 25
Db      89 GAGATCAAGCAAAATATAAATTAGTCTGAGTTAGTTCGAGGAGAGTTTCGGTGTGACG 148
Qy      26 TyrLeuCystrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerLysArg 45
Db      149 TATCTGTGCACGAGATCGAGACCGAGAGATTTTCTCATGCAAAATCAATCTTAAAGAAG 208
Qy      46 LysLeuArgThrAlaValAspValGluAspValArgGluValThrIleMetSerThr 65
Db      209 AAGCTGAAACGTCGATTGATATAGAGACGCTTAAGAGAGAAAGTTGAGATCATGAGGCAA 268
Qy      66 LeuProGluHisProAsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrVal 85
Db      269 ATGCTGAAACATCTTAATATTGTTACTTTGAAAGAGACTTATGAGATGATAAAGCTGTG 328
Qy      86 HisLeuValMetGluLeuGluGlyGluLeuPheGlyArgIleValAlaArgGly 105
Db      329 CATTTGGTTATGGAGCTTTGTGAGGCGTGCAGCTTTTCGATAGGATGTTGCTAGAGGG 388
Qy      106 HistyThrGluArgAlaAlaAlaThrValAlaArgThrIleAlaGluValValArgMet 125
Db      389 CATTATACGAGAGAGCTGCTGCTTCGTTTATTAAACGATCATCGAGGTTGTCAGATG 448
Qy      126 CysHisValAsnGluValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsn 145
Db      449 TGTCTAATGATGGTGGTATGTCACAGAGATTTAAACCTGAGAACTTCTTGTGTCAAAC 508
Qy      146 LysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysPro 165
Db      509 AAGAAGGAACCTGCATCTTTAAAGGCTATTAAATTAAGTCTCTCTGTATACATTAACCA 568
Qy      166 GlyGluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluValLysLys 185
Db      569 GCGAGAAATTTAAACGAAATTTCTTGGGAGTCTTACTATACATGGCTCCTGAAAGTATTAAG 628
Qy      186 ArgAsnTyrGlyProGluValAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeu 205
Db      629 AGGAGTCATGCAAGACATTCACATTTGGAGCGGAGGAGTCTCTACATATGCTC 688
Qy      206 CysGlyValProProPheTrp-AlaGluThrGluGlnGlyValAlaLeuAlaIleLeuAr 225
Db      689 TGTGTGTCTCCACCTTTCTCGGCAAAACCGAATGAGTTCGCAAAAGCAATTTCTTAA 748
Qy      225 gGlyValLeuAspPheLysArgAspProTrpSerGlnIleSerGlnAlaLysSerLe 245
Db      749 ATCTGTAATTAACTTTAAAGAGACCCCTGGCTTAAAGTTTCTGATAATGCAAAAGATCT 808
Qy      245 uValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGlnGlnValLeuAs 265
Db      809 GATCAAAAGAGTCTTCATCCTGATCCAAAGGCGTCTTAACCTGCTCAACCAAGTCTTGA 868
Qy      265 pHisProTrpIleGlnAsnAlaLys 273
Db      869 TCATCCGTGGATACAGAATGGTAAG 893

RESULT 7

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BU003544
LOCUS       OGG35J03.yg.ab1 QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
            OGG35J03, mRNA sequence.
ACCESSION   BU003544
VERSION     BU003544.1
KEYWORDS    EST.
SOURCE      BU003544.1 GI:22437939
            Lactuca sativa
            Lactuca sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
            Cichorieae; Lactuca.
REFERENCE   1 (bases 1 to 768)
            Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Riesberg,L.,
            Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J.,
            Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,
            Lai,Z., Church,S., Jackson,L. and Bradford,K.
            Lettuce and Sunflower ESTs from the Compositae Genome Project
            http://compgenomics.ucdavis.edu/
            Unpublished (2002)
            Contact: Alexander Kozik [R.W.Michelmore]
            Department of Vegetable Crops, R.W.Michelmore Lab
            University of California at Davis (UCD)
            Asmudson Hall, UCD, Davis, CA 95616, USA
            Tel: 1-(530)-742-1742
            Fax: 1-(530)-752-9659
            Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
            belongs to contig QG_CA_Contig5725, see http://cgpdb.ucdavis.edu/
            for details.
FEATURES             Location/Qualifiers
     source           1..768
                     /organism="Lactuca sativa"
                     /mol_type="mRNA"
                     /cultiivar="L.serriola"
                     /db_xref="taxon:4236"
                     /clone="OGG35J03"
                     /lab_hosts="E.coli"
                     /clone_lib="QG_EFGHJ lettuce serriola"
                     /note="vector: pBRCONASFIAB; The library was constructed
                     from 10 different sources of RNA from a single genotype.
                     Separate cDNAs were generated using primers that
                     incorporated unique 5' and 3' tags to distinguish each
                     source of RNA. cDNAs were then pooled, size-fractionated,
                     directionally cloned into a custom medium-copy vector and
                     transformations made with four size classes to minimize
                     size bias. Details of each source of RNA and library
                     construction can be obtained at http://cgpdb.ucdavis.edu/
                     TAG_TISSUE=germinating seeds
                     TAG_LIB=QG_EFGHJ lettuce serriola
                     TAG_SEQ=TCGTGCGGG"

ORIGIN
Alignment Scores:
  3.64e-113      Length: 768
Pred. No.:      Matches: 192
Score:          1042.00
Percent Similarity: 89.17%   Conservative: 22
Best Local Similarity: 80.00% Mismatches: 26
Query Match:     73.43%     Indels: 0
DB:              5          Gaps: 0

US-08-989-881-2 (1-274) x BU003544 (1-768)

Qy      6 GlnileSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGlyGluPheGlyIleThr 25
Db      49 GAGATTCAGCAAACTTATGTTCTTGTGTAAGAAATTTGGCAGAGAGAAATTTGGCATTA 108
Qy      26 TyrLeuCystrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerLysArg 45
Db      109 TATATGTGTACAGATAAGTCAACTGGTGAATTTTTCGTTGTAATCGATATCCAAAAG 168
Qy      46 LysLeuArgThrAlaValAspValGluAspValArgGluValThrIleMetSerThr 65

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Db      169  AGTTGAGGACTAGGTTGATATCGAGGATGTTAGGAGAGAGTTGAGATCATGGAGCAT 228
Qy      66  LeuProGluHisProAsnValVallysLeuLysAlaThrTyrGluAspAsnGluThrVal 85
Db      229  ATGCCTACTCACCTAATATCGTCCTTTGAAAGACACATACGAGATGATAGTGTCTTT 288
Qy      86  HisLeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArgIleValAlaArgGly 105
Db      289  CATTGGTTCATGGAGCTGTCGAGGAGGAGAGATTAATCGATCGGATTTGTCAGAGGC 348
Qy      106  HisTyrThrGluArgAlaAlaThrValAlaThrIleAlaGluValValArgMet 125
Db      349  CACTACACGAGAGAGCCCGCGGCTCACAGGACCATCGTCGAAATCATTCAGATG 408
Qy      126  CysHisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsn 145
Db      409  TGCCACAGCATGGTGTATGTCATCGTATCTTAAACCCGAAACCTTTTGTGTGCAAC 468
Qy      146  LysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysPro 165
Db      469  AAGAAGAACACAGCAGCTTTAAAGCTATGTATTTGGGTATPCCGTTTCTTCAAACCA 528
Qy      166  GlyGluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluValLeuLys 185
Db      529  GCGGAGAGGTTTAAACGAATTTAGGCAGTCCATACATGCTCCTCAGGTCCTTAA 588
Qy      186  ArgAsnTyrGlyProGluValAspValTrpSerAlaGlyValIleLeuTyrIleLeu 205
Db      589  AGAAACTATGGCCAGAGTTCAGCTATGAGTGCAGGGGTAATCTTGTACATATTGCTT 648
Qy      206  CysGlyValProPheThrAlaGluThrGluGlnGlyValAlaLeuAlaIleLeuArg 225
Db      649  TGTGAGTCCCTCCATTTTGGGAGAACTGAGCAAGAGTGTGCACAACTATTATCGA 708
Qy      226  GlyValLeuAspPheLysArgAspProTrpSerGlnIleSerGluSerAlaLysSerLeu 245
Db      709  TCAGTTGTAGATTTTAAAGGGATCCATGGGCCAGGATCTGTATGACCTAAAGATCTT 768

RESULT 8
CK250764 721 bp mRNA linear EST 30-JUL-2004
LOCUS EST734401 potato callus cDNA library, normalized and full-length
DEFINITION Solanum tuberosum cDNA clone POCB139 5' end, mRNA sequence.
ACCESSION CK250764
VERSION CK250764.1 GI:39803147
KEYWORDS Solanum tuberosum (potato)
SOURCE Solanum tuberosum
ORGANISM Solanum tuberosum
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE asterids; lamids; Solanales; Solanaceae; Solanum.
JOURNAL 1 (bases 1 to 721)
COMMENT Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
Generation of ESTs from potato callus tissue
Unpublished (2003)
Other ESTs: EST734402
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
1..721
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
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/clone="POCB139"
/tissue_type="callus"
/lab_host="DH10B-TonA"

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/clone_lib="potato callus cDNA library, normalized and
full_length"
/notes="Vector: pCMVSPORT6.1; Site_1: EcoRI; Site_2: NotI;
supplier: RNA was isolated from Solanum tuberosum var.
Kennebec callus tissue grown on solid media."

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ORIGIN

```

Alignment Scores:
Pred. No.: 1,648-109 Length: 721
Score: 1011.00 Matches: 188
Percent Similarity: 96.67% Conservative: 15
Best Local Similarity: 89.53% Mismatches: 7
Query Match: 71.25% Indels: 0
DB: 7 Gaps: 0

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US-08-989-881-2 (1-274) x CK250764 (1-721)

```

Qy      4  GlnThrGlnIleSerAspLysTyrIleLeuGlyValArgGluLeuGlyArgGlyGluPheGly 23
Db      90  AAAACATGCATATCTGACAAATACATCTTAGACACGAACTGGGTGGGGCGAATTTGGA 149
Qy      24  IleThrTyrLeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSer 43
Db      150  GTGACTTACCTTTGACCCGACAGGAGACCCGAGATGCCCTTGTCTGCAAAATCTATTCA 209
Qy      44  LysArgLysLeuArgThrAlaValAspValGluAspValArgGluValThrIleMet 63
Db      210  AAGAAGAAGAGCTCCGAACAGCTGTGATATCGAAGATGTGAGAGAGAACTTGTCTATTATG 269
Qy      64  SerThrLeuProGluHisProAsnValValLysLeuLysAlaThrTyrGluAspAsnGlu 83
Db      270  TCAGCCCTCTCTGATCACCCTAATATTGTGAAGTTGAGAGCTACTTATGAGATATGAA 329
Qy      84  ThrValHisLeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArgIleValAla 103
Db      330  GCAGTTTCATCTTGTCTATGAGCTATGTCAAGGTGGGAGTATTTGATAGAATTTGAGCT 389
Qy      104  ArgGlyHisTyrThrGluArgAlaAlaThrValAlaArgThrIleAlaGluValVal 123
Db      390  AGAGGGCATTACAGTGAAGAGCTGCAGCTGGGTTGCCAGAACTGTTGCAGAGGTTGTA 449
Qy      124  ArgMetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPhe 143
Db      450  AGGATGTCTCATCTGTAATGGGGTCATGCATAGAGACTTGAACCTTGAGAAATTTCTGTTT 509
Qy      144  AlaAsnLysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPhe 163
Db      510  GCTAATAAGAAAGAGCATCTGCTCTCAAGGCCATCGATTTTGGCTATCTGTCTTTTC 569
Qy      164  LysProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluVal 183
Db      570  AAGCCTGTGTGAAGATTTCTCTGAGATTGTGGGAAGTCCATACATGACACAGAGGTG 629
Qy      184  LeuLysArgAsnTyrGlyProGluValAspValTrpSerAlaGlyValIleLeuTyrIle 203
Db      630  TTGAAGCGGAGTTATGGACCAAGAGTTGATATTGGAGTGGTGGTGTCTATCTCTTTATAT 589
Qy      204  LeuLeuCysGlyValProPheTrpAla 213
Db      690  TTGTTATGGGGTTCTCTCCATTTTGGGCT 719

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RESULT 9

CA264357

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

RESULT 9

CA264357

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

CA264357 711 bp mRNA linear EST 26-SEP-2003
SCQGLB2041E01.g LB2 Saccharum officinarum cDNA clone SCQGLB2041E01
5', mRNA sequence.

CA264357

CA264357.1 GI:35959325

EST.

Saccharum officinarum

Saccharum officinarum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.

1 (bases 1 to 711)

Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.

The libraries that made SUCST

Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

Contact: Arruda P

Centro de Biologia Molecular e Engenharia Genetica

Universidade Estadual de Campinas

Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1137

Fax: 55 19 3788 1089

Email: parruda@unicamp.br

Clone distribution: clone distribution information can be found

through the Brazilian Clone Collection Center (BCCC) at

http://www.bcccenter.fcav.unesp.br

Plate: 041 row: E column: 01

Seq primer: T7 Promoter Primer.

Location/Qualifiers

FEATURES

1..711

/organism="Saccharum officinarum"

/mol_type="mRNA"

/db_xref="taxon:4547"

/clone="SCGLB2041E01"

/lab_host="DH10B"

/clone_lib="LB2"

/note="Organ: Lateral buds from plants adult plants growing in greenhouse; Vector: pSport1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from [lateral buds from plants adult plants growing in greenhouse]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucst.lad.ic.unicamp.br/public>"

ORIGIN

Alignment Scores:

Pred. No.: 8,31e-109 Length: 711
Score: 1005.00 Matches: 192
Percent Similarity: 87.76% Conservative: 16
Best Local Similarity: 81.01% Mismatches: 29
Query Match: 70.82% Indels: 0
DB: 6 Gaps: 0

US-08-989-881-2 (1-274) x CA264357 (1-711)

Qy 31 ArgGluThrArgGluAlaLeuAlaCysLysSerIleSerLysArgLysLeuArgThrAla 50
Db 1 CCGGCTCAGGGAGGCGCTGGCCCTGCAAGTCCATCTCAAGAAAGAGCTCCGACCC 60
Qy 51 ValAspValGluAspValArgArgGluValThrIleMetSerThrLeuProGluHisPro 70
Db 61 GTTGACATCGAGGAGCTGCGCGGAGGTGGAGATCATGCCACCTCCCAAGACCCC 120
Qy 71 AsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrValHisLeuValMetGlu 90
Db 121 AACGTGTCAGCTCAGGAGACACCTTACGAGGACGACAATCGCGTNCACCTCGTCATGG 180
Qy 91 LeuCysGluGlyGlyLeuPheGlyArgIleValAlaArgGlyHisTyrThrGluArg 110
Db 191 CTCTGTGAGGGCGGGAGCTCTTCGACCGCATCGTGGCGGGGACATACACTGAGGCG 240
Qy 111 AlaAlaAlaThrValAlaArgThrIleAlaGluValValArgMetCysHisValAsnGly 130
Db 241 GCTGCGCTTGGTCACAGCAGCTATCTGCGAGGTCTGTCAGATGTGCGCATAGCATGA 300
Qy 131 ValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsnLysLysGluAsnSer 150
Db 301 GTGATGCACAGGGATCTCAAAACCAAGAAATTTCTTTGTTGGCAACAAGAAATCAGCA 360

Qy 151 AlaleuLysAlaIleAspPheGlyLeuSerValLeuPheLysProGlyGluArgPheThr 170
Db 361 GCCCTTAAGGCCATTGATTTGGCTCTGTGTATTTTCACTCCAGGCGAAACGGTTTACT 420
Qy 171 GluIleValGlySerProTyrTyrMetAlaProGluValLeuLysArgAsnTyrGlyPro 190
Db 421 GAGATTGTTGGAAGTCTTATTACATGGCTCCAGAGGTGCTAAAGAGAAATATATGGCCCA 480
Qy 191 GluValAspValTrpSerAlaGlyValIleLeuTyrIleLeuLysGlyValProPro 210
Db 481 GAGGTTGATGTTNTGAGCTGCAGGAGTGATTTCTGTACATTTCTTCTTGTGTGCTCCTCCA 540
Qy 211 PheTrpAlaGluThrGluGlnGlyValAlaLeuAlaIleLeuArgGlyValLeuAspPhe 230
Db 541 TTCTGGGCGAAGAACGGAACAGGGGTGTNGCTCAGCAATTTATCCGATCTGCCATTGATTTC 600
Qy 231 LysArgAspProTrpSerGlnIleSerGluSerAlaLysSerLeuValLysGlnMetLeu 250
Db 601 AAAGAGATCCATGCCCAAGGGTGTCTGGATACGCCCAAGAACTTGTCCAGAGGAATGCTC 660
Qy 251 GluProAspSerThrLysArgLeuThrAlaGlnGlnValLeuAspHisPro 267
Db 661 AATCCGGANTCCAAACGACGATGCAGCTCAGCAAGTGTGTGATCACCCA 711

RESULT 10

CK281626 982 bp mRNA linear EST 02-AUG-2004
LOCUS EST744348 Nicotiana benthamiana mixed tissue cDNA library,
DEFINITION normalized, full-length Nicotiana benthamiana cDNA clone NBMA557 5'
end, mRNA sequence.
CK281626
CK281626.1 GI:39852434
EST.
KEYWORDS Nicotiana benthamiana
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
REFERENCE 1 (bases 1 to 982)
AUTHORS Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskiewicz, B., Jin, H. and Baker, B.
TITLE Generation of EST sequences from Nicotiana benthamiana
JOURNAL Unpublished (2003)
COMMENT Other ESTs: EST744346 EST744347 EST744349
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via <http://genome.arizona.edu/orders/>.
Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES

source

1..982
/organism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NBMA557"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/notes="vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN

Alignment Scores:

Pred. No.: 1,73e-108 Length: 982
 Score: 1004.00 Matches: 185
 Percent Similarity: 86.59% Conservative: 28
 Best Local Similarity: 75.20% Mismatches: 33
 Query Match: 70.75% Indels: 0
 DB: 7 Gaps: 0

US-08-989-881-2 (1-274) x CK281626 (1-982)

Qy 4 GlnThrGlnIleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGluPheGly 23
 Db 238 AAATCGAATATCGAGGAATATATCTAGTTGATAGAGATTAGGAGAGGTGATTCGGA 297
 Qy 24 IleThrTyrLeuGlySerThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSer 43
 Db 298 ATAACCTACCTCTGTACCGATCGTAACAGCAGTGAATTTGGCTTGCAGTCAATTCG 357
 Qy 44 LysArgLysLeuArgThrAlaValAspValGluAspValArgArgGluValThrIleMet 63
 Db 358 AAGCGAAACTTAGAACATCTGTGTATATAGAGGATGTAAGCGAGAGAGTGGCGATAATG 417
 Qy 64 SerThrLeuProGluHisProAsnValValLysLeuLysAlaThrTyrGluAspAsnGlu 83
 Db 418 AAGCATTTCCGTTAGATTCGAGCATTTGAGATTCAGAGAGCTGTGAGGATGAGAT 477
 Qy 84 ThrValHisLeuValMetGluLeuGlyGluGlyGluGlyGluPheGlyArgIleValAla 103
 Db 478 CGCGTGCAATTTGGTTATGAGTTGTGCGAAGCGCGGAGCTGTTCGATAGGATAGTGGCG 537
 Qy 104 ArgGlyHisTyrThrGluArgAlaAlaThrValAlaArgThrIleAlaGluValVal 123
 Db 538 CGGGGGCATTCACGAGCGTCTGCTCGCGGTCTCATCGACGCTGTGGAAGTGGTG 597
 Qy 124 ArgMetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPhe 143
 Db 598 CAGCTTTGTCTAAGNATGTTGTGATTCATCAGACTTGAACTGAGAGCACTTTTGT 657
 Qy 144 AlaAsnLysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPhe 163
 Db 658 GCTAATAAAGGAGAAATTCGCACCTTAAGGCTATTGATTTGGTTTGTCCATATCTTC 717
 Qy 164 LysProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluVal 183
 Db 718 CAGCCAGGTGAGAGGTTTCTGAAATTTGTGAAGCCCTTATATATGCTCCTCAGGTG 777
 Qy 184 LeuLysArgAsnTyrGlyProGluValAspValTyrSerAlaGlyValIleLeuTyrIle 203
 Db 778 CTCAGCGGAACTATGGACCAGAAATAGATATATGAGTGCAGAGTCAATATATATAT 837
 Qy 204 LeuLeuGlyValProPheTrpAlaGluThrGluGlnGlyValAlaLeuAlaIle 223
 Db 838 TTGTTATGTGGAGTTCCTCCCTTTGGGCTGAATCTGAACAAGGTGTTGCTCAGGCGATC 897
 Qy 224 LeuArgGlyValLeuAspPheLysArgAspProTyrSerGlnIleSerGluSerAlaLys 243
 Db 898 TTACGTGGAGCAATAGATTTCAAGCGTGACCCCTGGCCGAGTATTTCAGAGACTCTCTACA 957
 Qy 244 SerLeuValLysGlnMet 249
 Db 958 AATCTTTACACAATG 975

RESULT 11

CK297575 899 bp mRNA linear EST 02-AUG-2004
 LOCUS EST760289 Nicotiana benthamiana mixed tissue cDNA library,
 DEFINITION normalized, full-length Nicotiana benthamiana cDNA clone NBMD981 5'
 end, mRNA sequence.
 CK297575
 ACCESSION CK297575.1 GI:39884099
 VERSION
 KEYWORDS EST.

SOURCE
ORGANISM

Nicotiana benthamiana
 Nicotiana benthamiana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Nicotiana.

REFERENCE

1 (bases 1 to 889)

AUTHORS

Buell, C.R., Hart, A., Ziemann, V., Karamycheva, S.A., Day, B.,

TITLE

Staskawicz, B., Jin, H. and Baker, B. Karamycheva, S.A., Day, B.,

JOURNAL

Generation of EST sequences from Nicotiana benthamiana

COMMENT

Unpublished (2003)

Other ESTs: EST760290

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@igr.org

Clones can be requested from the University of Arizona Genomics

Institute via <http://genome.arizona.edu/orders/>.

Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES

source

1..889

/organism="Nicotiana benthamiana"

/mol_type="mRNA"

/db_xref="taxon:4100"

/clone="NBMD981"

/tissue_type="abiotic and biotic stress-treated leaves,
 callus tissue and root tissue"

/lab_host="DH10B-Tona"

/library="Nicotiana benthamiana mixed tissue cDNA

/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;

supplier: RNA was isolated from Nicotiana benthamiana

tissues that include callus, roots from liquid culture

grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),

cold-stressed leaves (5 C 3 hr, 6hr), and pathogen

challenged leaves (Pseudomonas syringae pv tomato 12 hr;

Xanthomonas campestris pv campestris 12 hr, 18hr;

Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas

campestris pv vesicatoria 18hr). RNA was isolated from

these tissues and pooled in approximately equal molar

amounts."

ORIGIN

Alignment Scores:

Pred. No.: 4,05e-102 Length: 889
 Score: 950.00 Matches: 175
 Percent Similarity: 87.39% Conservative: 26
 Best Local Similarity: 76.09% Mismatches: 29
 Query Match: 66.95% Indels: 0
 DB: 7 Gaps: 0

US-08-989-881-2 (1-274) x CK297575 (1-889)

Qy 4 GlnThrGlnIleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGluPheGly 23
 Db 199 AAATCGAATATCGAGGAATATATCTAGTTGATAGAGATTAGGAGAGGTGATTCGGA 258
 Qy 24 IleThrTyrLeuGlySerThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSer 43
 Db 259 ATAACCTACCTCTGTACCGATCGTAACAGCAGTGAATTTGGCTTGCAGTCAATTCG 318
 Qy 44 LysArgLysLeuArgThrAlaValAspValGluAspValArgArgGluValThrIleMet 63
 Db 319 AAGCGAAACTTAGAACATCTGTGTATATAGAGGATGTAAGCGAGAGAGTGGCGATAATG 378
 Qy 64 SerThrLeuProGluHisProAsnValValLysLeuLysAlaThrTyrGluAspAsnGlu 83
 Db 379 AAGCATTTCCGTTAGATTCGAGCATTTGAGATTCAGAGAGCTGTGAGGATGAGAT 438
 Qy 84 ThrValHisLeuValMetGluLeuGlyGluGlyGluGlyGluPheGlyArgIleValAla 103
 Db 439 CGCGTGCAATTTGGTTATGAGTTGTGCGAAGCGCGAGCTGTTCGATAGGATAGTGGCG 498
 Qy 104 ArgGlyHisTyrThrGluArgAlaAlaThrValAlaAlaThrIleAlaGluValVal 123


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Db 499 CGGGGGATTACACGGACGGTCTGCGCGCTCATCGCGACGGTGTGGAAGTGGT 558
Qy 124 ArgMetCysHisValAsnGlyValMetHisArgAspLeuTyrProGluAsnPheLeuPhe 143
Db 559 CAGCTTTGTCATAGAATGGTGTGATCATCGAGACTTGAAACCTGAGAACTTTTGT 618
Qy 144 AlaAsnLysLysGluAsnSerAlaLeuLysAlaLeuAspPheGlyLeuSerValLeuPhe 163
Db 619 GCTAATAAAGAGGAAATTCGCCACTTAAGGCTATTGATTTGGTTTGTCTCATATTC 678
Qy 164 LysProGlyGluArgPheThrGluLeuValGlySerProTyrTyrMetAlaProGluVal 183
Db 679 CAGCCAGGTGAGAGGTTTCTGAAATTTGGAAGCCCTTATTATATGCGCTCTGAGGT 738
Qy 184 LeuLysArgAsnTyrGlyProGluValAspValTyrSerAlaGlyValLeuTyrLeu 203
Db 739 CTCAGCGCAACTATGACCAAGAAATAGATATATGAGTGCAGGAGTCATTATGAT 798
Qy 204 LeuLeuCysGlyValProProPheTyrAlaGluThrGluGlnGlyValAlaLeuAla 223
Db 799 TTGTTATGTGGAGTTCCTCCCTTTTGGGCTGAATCTGAACAAGGTGTGCTCAGGCCATC 858
Qy 224 LeuArgGlyValLeuAspPheLysArgAsp 233
Db 859 TTACGTGGAGCAATAGATTTCAAGCGTGAA 888

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RESULT 12
CB894498 864 bp mRNA linear EST 24-APR-2003
LOCUS CB894498
DEFINITION CB894498 HOGA Medicago truncatula cDNA clone HOGA-31K18, mRNA
sequence.

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ACCESSION CB894498
VERSION CB894498.1 GI:30101667
KEYWORDS EST.
SOURCE Medicago truncatula (barrel medic)

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ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.

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REFERENCE 1 (bases 1 to 864)
AUTHORS Hahn,M.G., Ojanen-Reuhs,T., Samac,D., Town,C.D., Van Aken,S.,
Utterback,T., Cho,J. and Fraser,C.M.
TITLE ESTs from roots of Medicago truncatula treated with
oligogalacturonides of DP 6-20
JOURNAL Unpublished (2001)
COMMENT Contact: Michael G. Hahn
Complex Carbohydrate Research Center
University of Georgia
220 Riverbend Road, Athens, GA 30602-4712, USA
Tel: 706-542-4457
Fax: 706-542-4412
Email: hahn@ccr.uga.edu
TIGR sequence name: MTWDT69TK
More information is available at: www.medicago.org

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Seg primer: Skmod (CTA GAA CTA gTg GAT CC).
Location/Qualifiers
1..864
/organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:3890"
/culture="A17"
/tissue_type="3 day old seedling roots"
/dev_stage="24 hours after treatment in the dark at 26 C
with 0.5 mg/ml oligogalacturonides (DP 6-20) in the
presence of 100 ug/ml Gentamicin"
/lab_host="XLOLR"
/clone_lib="HOGA"
/notes="Vector: pluescript SK-; Site 1: EcoRI; Site 2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from

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FEATURES

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source

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RESULT 13
LOCUS CB266323
DEFINITION

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ACCESSION CA266323
VERSION CA266323.1 GI:35965079
KEYWORDS EST.
SOURCE Saccharum officinarum

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ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum

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CA266323 688 bp mRNA linear EST 26-SEP-2003
SCAGLUB2046H03.g LB2 Saccharum officinarum cDNA clone SCAGLUB2046H03
5', mRNA sequence.

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ACCESSION CA266323
VERSION CA266323.1 GI:35965079
KEYWORDS EST.
SOURCE Saccharum officinarum

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ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum

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Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-zap phage using Ex-assist helper phage and propagated in SOLR cells."

ORIGIN

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Alignment Scores:
Pred. No.: 1.53e-101 Length: 864
Score: 945.00 Matches: 176
Percent Similarity: 89.55% Conservative: 21
Best Local Similarity: 80.00% Mismatches: 23
Query Match: 66.60% Indels: 0
DB: Gaps: 0
US-08-989-881-2 (1-274) x CB894498 (1-864)

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Qy 55 AspValArgArgGluValThrIleMetSerThrLeuProGluHisProAsnValValLys 74
Db 1 GATGTTGCGCGTGAAGTTGCTATCATCGCCATTTCGCCAAGAGTTCGAGTATTGTCA 60
Qy 75 LeuLysAlaThrTyrGluAspAsnGluThrValHisLeuValMetGluLeuLysGluGly 94
Db 61 CTTGCGTGAAGCGTGTGAGGATGATAATGCTGTTTCATCTTCTCATGAGAGCTTTGTGA 120
Qy 95 GlyGluLeuPheGlyArgIleValAlaArgGlyHisTyrThrGluArgAlaAlaThr 114
Db 121 GGGGAGCTTTTTCATCGGATTTGTAGAGGACATTATACGAGAGAGCGGCTCGCGC 180
Qy 115 ValAlaArgThrIleAlaGluValAlaArgMetCysHisValAsnGlyValMetHisArg 134
Db 181 GTTGGGAGGACGATTGTTGGAGGTTGTGCAGCTTTGTCATAAGCATGGGTTATTTCAT 240
Qy 135 AspLeuLysProGluAsnPheLeuPheAlaAsnLysLysGluAsnSerAlaLeuLysAla 154
Db 241 GATCTTAAGCGGAGAAATTTCTTTTGGGAATTAAGAAGGAGAAATTCGCCACTTTAA 300
Qy 155 IleAspPheGlyLeuSerValLeuPheLysProGlyGluArgPheThrGluLeuValGly 174
Db 301 ATTGATTTTGGGTGCTATTTCTTTAAAGGAGTGAAGAAATTCAGAAATTTGTTGA 360
Qy 175 SerProTyrTyrMetAlaProGluValLeuLysArgAsnTyrGlyProGluValAspVal 194
Db 361 AGTCCATATTATACATGCTCCAGAGGTGCTCAAGCGGAACTATGGACCTGAAATAGATA 420
Qy 195 TrpSerAlaGlyValIleLeuTyrIleLeuLysCysGlyValProProPheTyrAlaGlu 214
Db 421 TGGAGTGCAGGAGTGATCTTATATCTTATTTGCGGTGTTCCCGCTTTTGGGCTGAA 480
Qy 215 ThrGluGlnGlyValAlaLeuAlaLeuArgGlyValLeuAspPheLysArgAspPro 234
Db 481 TCTGAGCAAGGAGTTTGCACAGCTATTCTTCGAGGCGCTTATAGATTTCAACCGGAAC 540
Qy 235 TrpSerGlnIleSerGluSerAlaLysSerLeuValLysGlnMetLeuGluProAspSer 254
Db 541 TGGCCCAAGTATTCTGAAAGTGTCTAAAGTCTTTGTTAAGCAATTTTGGAAACAGAC 600
Qy 255 ThrLysArgLeuThrAlaGlnGlnValLeuAspHisProTyrIleGlnAsnAlaLysLys 274
Db 601 AAGCTTCGATTAAACGCCAAACAAAGTCTTTGAGCATCTCTTGGCTCCAAAATGCTAAG 660

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361 Db      |||||GGCCTTAAGGCCATTGATTTTGGCCCTGTCTGATTTTTTCACTCAGCGGAACGGTTTACT 420
171 Qy      GluIleValGlySerProTyrTyrMetAlaProGluValLeuLysArgAsnTyrGlyPro 190
         ::::|
421 Db      GAGATTGTTGGAAGTCCTATTACATGGCTCCAGAGGTGCTAAAGAACAATTTATGGCCA 480
191 Qy      GluValAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeuCysGlyValProPro 210
         ::::|
481 Ab      AAGGTTTGATGTTTGGAGTCGAGAGTGATCTGTACATCTCTCTTTGGTGTCCCTCCA 540
211 Qy      PheTToAlaGluThrCluGlnGlyValAlaLeuAlaIleLeuArgGlyValLeuAspPhe 230
         |||||
541 Db      TTCTGGGCAGAACCGAACCAGGTGTGTCTCAGGCAATTATCCGATCTGCCATTGATTTC 600
231 Qy      LysArgAspProTrpSerGlnIleSerGluSerAlaLysSerLeuValLysGlnMetLeu 250
         ::::|
601 Ab      AAAAGAGATCCATGGCAGAGGTGTCTGATTACGCCCAAGAACCTTGTCCAGAGGAATGCTC 660
251 Qy      GluProAspSerThrLysArgLeuThr 259
         |||||
661 Db      AT-CCGGATCCAAAACGACGATTGACA 686

RESULT 14
BQ148394
LOCUS       BQ148394
DEFINITION   Medicago truncatula (barrel medic)
ACCESSION   BQ148394
VERSION     BQ148394.1 GI:20285453
KEYWORDS    EST.
SOURCE      Medicago truncatula (barrel medic)
ORGANISM    Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; euroids 1; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1 (bases 1 to 679)
AUTHORS    Torres-Jerez,I., Scott,A.D., Harris,R.A., Gonzales,R.A., Bell,C.J.,
            Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.
TITLE       Expressed Sequence Tags from the Samuel Roberts Noble Foundation
JOURNAL     Medicago truncatula flower library
COMMENT     Unpublished (2001)
            Contact: May GD
            Plant Biology Division
            The Samuel Roberts Noble Foundation
            2510 Sam Noble Parkway, Ardmore, OK 73402, USA
            Tel: 580 224 6650
            Fax: 580 224 6692
            Email: gdmay@noble.org
            Insert Length: 679 Std Error: 0.00
            Plate: 067 Row: H Column: 06
Seq primer: TCACACGAGAAACAGCTATGAC.
            Location/Qualifiers
                1..679
                   /organism="Medicago truncatula"
                   /mol_type="mRNA"
                   /db_xref="taxon:3880"
                   /clone="NF067H06FL"
                   /tissue_type="Developing flowers"
                   /dev_stage="Developmentally pooled. Contains a mixture of
very young, developing, fully-opened flowers and flowers
in early transition into pods."
                   /clone_lib="Developing flower"
                   /note="Vector: Lambda Zap; cDNA was prepared from polyA+
enriched, pooled samples of equivalent amounts of total
RNA from very young, developing, fully-opened flowers and
flowers transitioning into pods. The cDNA was
directionally ligated into the Uni-Zap XR vector
(Stratagene) and packaged using the Gigapack III Gold
packaging extracts. Phagemids containing cDNA inserts were
in vivo excised from the recombinant Uni-Zap XR vector
using EXassist helper phage and the E. coli strain
```

XL1-Blue MRF' (Stratagene). Excised plasmids were plated using SOLR cells."

ORIGIN

Alignment Scores:
 Pred. No.: 4.29e-101 Length: 679
 Score: 940.00 Matches: 176
 Percent Similarity: 88.34% Conservative: 21
 Best Local Similarity: 78.92% Mismatches: 25
 Query Match: 66.24% Indels: 1
 DB: 5 Gaps: 0

US-08-989-881-2 (1-274) x BQ148394 (1-679)

Qy 6 GlnIleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGlyGluPheGlyIleThr 25
 Db 11 GAGATATTACAAACATTCGAATTTAGGGAGAGAAATTTAGGAGAGAGAAATTTGGAAATAACG 70
 Qy 26 TyrLeuGlyThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerLysArg 45
 Db 71 TATTATGTAAGATAGAGAAACGGGAGAGGAAATTTAGCTTGTAAATCGATTTCAAGGAT 130
 Qy 46 LysLeuArgThrAlaValAspValGluAspValArgArgGluValThrIleMetSerThr 65
 Db 131 AAGCTAAGAACACGCGATTTGATATTCAGATGTTAGACAGAGAGCTTGAATATATGAGGCAT 190
 Qy 66 LeuProGluHisProAsnValLysLysLeuLysAlaThrTyrGluAspAsnGluThrVal 85
 Db 191 TTACCTAAACATCTCTAATATTGTTTACGTTGAAGGATCTTTATGAAGATGATGATATCTT 250
 Qy 86 HisLeuValMetGluLeuGlyGlyGluLeuPheGlyArgIleValAlaArgGly 105
 Db 251 CATCTTGTATGGAGCTTTGTGAAGTGTGAGCTTTTGTATCGGATTTGCTTAAGGGA 310
 Qy 106 HisTyrThrGluArgAlaAlaThrValAlaArgThrIleAlaGluValValArgMet 125
 Db 311 CATTATACCGAACGCGCGCGCGCGTGTGTTAAGACCATCGTTCAAGTGTTCAGATG 370
 Qy 126 CysHisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsn 145
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 Qy 146 LysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysPro 165
 Db 431 AAGAAGGAACATCACCTTTGAAAGCTATTGACTTTGTTGTTGCTCAATTTAAACCA 490
 Qy 166 GlyGluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluValLeuLys 185
 Db 491 GGTGATAAATTTAAGAGATAGTTGGGAGTCCATATTACATGCGNCCCTGAAGATTTGAAG 550
 Qy 186 ArgGluGlyProGluValAspValTrpSerAla-GlyValIleLeuTyrIleLeuLe 205
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 Qy 205 uCysGlyValProProPheTrpAlaGluThrGluGlnGlyValAlaLeuAlaIleLeuAr 225
 Db 611 TTGTGTATCTCTCTCTTTTGGGCANAACTGAGCAGGGAATTTGCTCAAGCAATTTATAG 670
 Qy 225 gGlyVal 227
 Db 671 ATCCGTT 677

RESULT 15

CV470355 914 bp mRNA linear EST 01-OCT-2004
 LOCUS
 DEFINITION 43200.1 Common 'Scab'-Challenged Tubers Solanum tuberosum cDNA clone
 43200 5', mRNA sequence.
 ACCESSION CV470355
 VERSION CV470355.1 GI:53695131
 KEYWORDS EST.
 SOURCE Solanum tuberosum (potato)
 ORGANISM Solanum tuberosum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE
AUTHORSTITLE
JOURNAL
COMMENT

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Solanum.
 1 (bases 1 to 914)
 Flinn,B., Rothwell,C., Sardana,R., Griffiths,R., Lague,M., De
 Koeyer,D., Audy,P., Goyer,C., Li,X.-Q., Wang-Pruski,G. and Regan,S.
 Generation of ESTs from common scab-challenged potato tubers
 Unpublished (2004)
 Contact: Barry Flinn
 The Canadian Potato Genome Project - BioAtlantech
 921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA
 Email: bflinn@bioatlantech.nb.ca
 Seq primer: T3.

FEATURES

source

1..914
 Location/Qualifiers
 /organism="Solanum tuberosum"
 /mol_type="mRNA"
 /cultivar="Shepody"
 /db_xref="taxon:4113"
 /clones="43200"
 /tissue_type="Tubers"
 /lab_host="XL10-Gold"
 /clone_lib="Common Scab-Challenged Tubers"
 /notes="vector: pBluescript II SK(+); XR; Site_1: EcoRI;
 Site_2: XhoI; supplier: Pathogen-challenge series. Tubers
 from pathogen-free Solanum tuberosum var. Shepody, clone
 1756, were inoculated with Streptomyces scabei EF-35, by
 applying 1 ml of a spore stock (OD650 = 0.7). Tubers were
 placed in trays of sand and watered from the bottom for
 the remainder of the experiment. Inoculated tubers were
 sampled at 2 days, 1 week, 2 weeks and 4 weeks
 post-infection. Harvested tubers were washed in distilled
 water, blotted dry, cut into small pieces and frozen in
 liquid nitrogen. RNA was isolated from each sample
 collection, pooled and used for cDNA library
 construction."

ORIGIN

Alignment Scores:

Pred. No.: 9.87e-101 Length: 914
 Score: 938.50 Matches: 195
 Percent Similarity: 81.34% Conservative: 23
 Best Local Similarity: 72.76% Mismatches: 42
 Query Match: 66.14% Indels: 9
 DB: 7 Gaps: 2

US-08-989-881-2 (1-274) x CV470355 (1-914)

Qy 15 ArgGluLeuGlyArgGlyGluPheGlyIleThrTyrLeuGlyThrAspArgGluThrArg 34
 Db 1 AGAGAGTTAGGAGGAGGAGAAATC-GGGATAACTTACCTTTGTATAGATCGTAGCAGTAGG 59
 Qy 35 GluAlaLeuAlaCysLysSerIleSerLysArgLysLeuArgThrAlaValAspValGlu 54
 Db 60 GAACCTTTGGCTGTAAAGTCGATTTCCGAAACGGGAAGTTACGACAGAGTGGATGGAG 119
 Qy 55 AspValArgArgGluValThrIleMetSerThrLeuProGluHisProAsnValLys 74
 Db 120 GATGTAGGAGAGAGAGTGGCAATTTATCAAGCATTTGCCACAGAAATTCAGATTTGTGAGT 179
 Qy 75 LeuLysAlaThrTyrGluAspAsnGluThrValHisLeuValMetGluLeuGlyGly 94
 Db 180 TTTAAGGAAGCGTGTGAGGATGAAATGCTGCTTCATTTGGTGTGAGCAATATGTGAGGT 239
 Qy 95 GlyGluLeuPheGlyArgIleValAlaArgGlyHisTyrThrGluArgAlaAlaAlaThr 114
 Db 240 GGTGAGCTGTTTGTATAGGATCGTTGCTAGGGGGCATTTATCTGAACGAGCAGCTGCTGCT 299
 Qy 115 ValAlaArgThrIleAlaGluValValArgMetCysHisValAsnGlyValMetHisArg 134
 Db 300 GTTACACGACGATTTGTGGAGTTGTGCAGCTTTGTCCAAACATGAGTGATTCATAGA 359
 Qy 135 AspLeuLysProGluAsnPheLeuAlaAsnLysLysGluAsnSerAlaLeuLysAla 154

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Qy      175 SerProTyrTyrMetAlaProGluValLeuLysArgAsnTyrGlyProGluValAspVal 194
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Qy      215 ThrGluGlnGlyValAla-LeuAlaIleLeuArgGlyValLeuAspPheLys-ArgAsp- 233
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Qy      253 AspSerThrLysArgLeuThr-----AlaGlnGlnValLeuAspHisPro-TrpIle-G 270
Db      720 CAAGATCCAAAGGCTTCGACTGACTGCAAAAGCAAGTACTTTTCAGCACCCCTTTGGGTTC 779
Qy      270 LysAlaLysLys 274
Db      780 AAAATGCTAAGAA 793
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